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OM nucleic - nucleic search, using sw model

Run on: January 6, 2004, 23:20:54 ; Search time 922 Seconds
(without alignments)
10399.570 Million cell updates/sec

Title: US-09-750-240-10
Perfect score: 3552
Sequence: 1 atgtcatggttagtgcc.....aaggaccagggtggcact 3552

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq 19Jun03:*

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25:	/SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3552	100.0	3552	22	AAD08567 Human cardiac aden
2	3552	100.0	3552	24	ABSS54137 Human cDNA encodin
3	3545.6	99.8	4942	20	AA000461 Human type VI aden
4	3484.8	98.1	3549	22	AAD08563 Human cardiac aden
5	3484.8	98.1	3549	22	ABSS54133 Human cDNA encodin
6	3443.2	96.9	3582	22	AAD08568 Human modified car
7	3443.2	96.9	3582	24	ABSS54138 Chimaeric cDNA enc
8	3057.6	86.1	4046	14	AAQ42525 Cardiac adenylcyl c

9	2816.2	79.3	5841	24	ABI99680 Mouse ischaemic co
10	2810.4	79.1	4131	21	AAAS3923 Type VI adenylcyl c
11	1763.4	49.6	1812	22	AAD08562 Human partial card
12	1763.4	49.6	1812	24	ABSS54132 Human cDNA encodin
13	1763.4	49.6	2127	19	AAV23246 Human adenylcylcyl
14	1761	49.6	4523	20	AA00462 Human type V aden
15	1750.8	49.3	4356	16	AAQ95540 Cardiac adenylcyl c
16	1749.2	49.2	4356	14	AAQ37543 Cardiac adenylcyl c
17	1696.2	47.8	3924	21	AAAS3922 Type V adenylcyl c
18	886.2	24.9	3137	24	AAD28058 Human adenylcyl and
19	604.4	17.0	3978	21	AAAS3918 adenylcyl cyclase t
20	590.8	16.6	837	22	AAS30177 DNA encoding rena
21	542	15.3	3811	24	AAD28061 Human adenylcyl and
22	528.6	14.9	915	22	AAS30223 DNA encoding rena
23	528.6	14.9	915	22	AAS27146 cDNA encoding nove
24	512.4	14.4	3518	22	AA02694 Human adenylate cy
25	510	14.4	6005	25	ABX10417 DNA encoding prote
26	498.6	14.0	6470	24	AAD31191 Human adenylate cy
27	497	14.0	4011	22	AAD06820 Human adenylate cy
28	493	13.9	6196	24	AAD41270 Human adenylate cy
29	492.4	13.9	3243	24	AAAD1265 Human adenylate cy
30	485.2	13.7	4601	21	AAAS3925 Type VIII adenylcyl
31	476.6	13.4	4827	23	ABL07501 Drosophila melanog
32	474.8	13.4	5873	24	AAD31190 Human adenylate cy
33	465.8	13.1	3769	24	AAD28057 Human adenylcyl and
34	458.6	12.9	4008	17	AAT14528 Rat adenylcyl cycla
35	458.6	12.9	4008	17	AAAS3919 Adenylcyl cyclase t
36	456.2	12.8	2731	25	ACA56746 Signalling pathway
37	456.2	12.8	3312	24	ABN89298 Human adenylate cy
38	455.4	12.8	4533	21	AAAS3920 Type III adenylcyl
39	449.4	12.7	5199	21	AAAS3924 Type IV adenylcyl
40	431	12.1	3357	21	AAAS3921 Type IV adenylcyl c
41	424.8	12.0	4355	24	ABL39754 Human NS cDNA sequ
42	416.8	11.7	3505	24	ABL34078 Human secreted pro
43	408.2	11.5	2601	21	AAC99124 Human pancreatic c
44	399.6	11.2	4080	22	AAL16647 Human cDNA sequenc
45	389.8	11.0	1652	21	AAAS3926 Adenylcyl cyclase C

ALIGNMENTS

RESULT 1

AAAD08567	ID	AAD08567	standard; DNA; 3552 BP.
AAAD08567	AC	AAD08567	
AAAD08567	XX	04-SEP-2001	(first entry)
AAAD08567	DT	Human cardiac adenylcylase VI (ACVI) isoform #2 DNA.	
AAAD08567	DE	Human; cardiac; beta-adrenergic signalling protein; beta-ASP; myocardi	
AAAD08567	KW	cardium; gene therapy; beta-adrenergic receptor; beta-AR; adenylylcyclase; adenylylase kinase; GRK; heart disease; congestive heart failure;	
AAAD08567	KW	G-protein receptor kinase; GRK; heart disease; congestive heart failure;	
AAAD08567	KW	cardiac adenylcylase VI; ACVI isoform; beta-ASP transgene; ds.	
AAAD08567	XX	Homo sapiens.	
AAAD08567	XX	Key	Location/Qualifiers
AAAD08567	FH	CDS	1..3507
AAAD08567	FT		/*tag= a
AAAD08567	FT		/product= "Human cardiac adenylcylase VI isoform #2"
AAAD08567	FT		/EC_number= "4.6.1.1"
AAAD08567	XX	WO200148164-A2.	
AAAD08567	XX	05-JUL-2001.	
AAAD08567	XX	26-DEC-2000; 2000MO-US35411.	
AAAD08567	XX	27-DEC-1999; 99US-0472667.	

1681 GAGGAGAGGCGCATGCTGSCCAAGCTGACAGCGAATCTGGGCCAACTCCATGGAAGGGCTG 1740
1681 GAGGAGAGGCGCATGCTGSCCAAGCTGACAGCGAATCTGGGCCAACTCCATGGAAGGGCTG 1740
1741 ATGCCGCGCTGGGTTCTTGATCGTGCCTTCTCCGAGCAAGGACTCCAGGCGCTTCCGC 1800
1741 ATGCCGCGCTGGGTTCTTGATCGTGCCTTCTCCGAGCAAGGACTCCAGGCGCTTCCGC 1800
1801 CAGATGGGCAATGATGATTTCCAGCAAGAAAGCAACCGGGGCAACCAAGATGCCCTGAAACCTT 1860
1801 CAGATGGGCAATGATGATTTCCAGCAAGAAAGCAACCGGGGCAACCAAGATGCCCTGAAACCTT 1860
1861 GAGGATGAGGTGAGTTCCTGAGCCGTCGATCGATCGATGCGCCGAGCATGATCAGCTG 1920
1861 GAGGATGAGGTGAGTTCCTGAGCCGTCGATCGATCGATGCGCCGAGCATGATCAGCTG 1920
1921 CGGAAGGACCAATGTCGCGCGGTTCTGCTCACTTCCAGAGAGAGATCTTGAGAGAG 1980
1921 CGGAAGGACCAATGTCGCGCGGTTCTGCTCACTTCCAGAGAGAGATCTTGAGAGAG 1980
1981 TACTCCCGAAGGTGGATCCCGCTTCGGAGCTTACGTTGCTGCTGCTGCTGCTGCTTTC 2040
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2041 TGCCTCATCTGCTTCATCAGCTTCTCATCTTCCACACTCCACCTGATGCTTGGATC 2100
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2101 TATGCCAGCATCTTCTGCTGCTGCTTATCAGCGTGTGCTGCTGCTGCTGCTGCTGCTG 2160
2161 GGTTCCTCTGTTCCCTAAGGCCCTGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
2161 GGTTCCTCTGTTCCCTAAGGCCCTGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
2221 CATAGCAGCGAGTGGCATCTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
2221 CATAGCAGCGAGTGGCATCTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
2281 ATGTTTCACTGTAAACACACCCCAATACGGAGCTGTGACGCCGATGCTGATTTAAACA 2340
2281 ATGTTTCACTGTAAACACACCCCAATACGGAGCTGTGACGCCGATGCTGATTTAAACA 2340
2341 CCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
2341 CCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
2401 CCCCTGTGTAGGGCAACATGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
2401 CCCCTGTGTAGGGCAACATGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
2461 CTGCTGAGTCTTCTGGCGAGCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
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2521 ATGATCTTTGCTTGGGGCTCATCTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580
2581 ATCTTTGACAATATGACCTACTGCTTGGCGTCCATGCTTGGCTTCTTCCATGAGACC 2640
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2641 TTTGATGGCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
2641 TTTGATGGCTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700
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3121 TCAGGGCTGAACCGCCAGCACTTACGATCAGGTGGGCCCTCCACATCATCTGCCCTGGCT 3180
3121 TCAGGGCTGAACCGCCAGCACTTACGATCAGGTGGGCCCTCCACATCATCTGCCCTGGCT 3180
3181 GACTACGCCATCGCGCTCATGAGCAGATGAAGACATCAATGAGCATCTCCTTCAACAT 3240
3181 GACTACGCCATCGCGCTCATGAGCAGATGAAGACATCAATGAGCATCTCCTTCAACAT 3240
3241 TTCCAGATGAAGATTGGGCTCAACATGGGCCAGCTGCTGGCAGGTGTATCGGGCTCGG 3300
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3301 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTGTATGACAGCAGC 3360
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3361 GGGGTCCCGACCGAATCCAGGTGACCGACCGACCTGTACCAAGGTCTAGCTGCCAAGGC 3420
3361 GGGGTCCCGACCGAATCCAGGTGACCGACCGACCTGTACCAAGGTCTAGCTGCCAAGGC 3420
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3421 TACCAGCTGGAGTGTCCGAGGGGTGTCAAGGTGAAGGGCAAGGGGAGATGACCACTAC 3480
3481 TTCTCTCAATGGGGGCCCGCAGAGTTAACAGGGGCCAGCCACAAATTCAGCTGAAGGGACC 3540
3481 TTCTCTCAATGGGGGCCCGCAGAGTTAACAGGGGCCAGCCACAAATTCAGCTGAAGGGACC 3540
3541 AAGGTGGGCACT 3552
3541 AAGGTGGGCACT 3552

RESULT 2

ABS54137

ID ABS54137 standard; cDNA; 3552 BP.

XX

AC AB854137;

XX

DT 20-NOV-2002 (first entry)

XX

DE Human cDNA encoding Adenylylase isoform 6, AC-VI, #2.

XX

Human; ss; gene; adenylylase isoform 6; AC-VI; CHF; gene therapy;

KW beta-adrenergic signalling protein; congestive heart failure; cardiant;

KW cardiac function; adenovirus vector; transgenic; gene therapy;

KW beta-adrenergic signalling protein; beta-ASP; heart disease.

XX

OS Homo sapiens.

XX

PH	Key	Location/Qualifiers	QY	121	CCCCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCAACCCCTCGGGCCCC	180
FT	CDS	1..3507	DB	121		180
FT		/+tag= a				
FT		/EC_number= "4.6.1.1"	QY	181	CCTCGGTGCCCTTGCAGGATGACGGCTTCATCCGAGGGGGGGCCAGGCAAGGCAAG	240
XX		/product= "Adenylylase isoform 6"	DB	181	CCTCGGTGCCCTTGCAGGATGACGGCTTCATCCGAGGGGGGGCCAGGCAAGGCAAG	240
XX	US2002103147-A1.		QY	241	GAGCTGGGGCTCGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGTGACACAGCAGCG	300
XX	01-AUG-2002.		DB	241	GAGCTGGGGCTCGGGCAGTGGCCCTTGGGCTTCGAGGATACCGAGTGACACAGCAGCG	300
XX	26-DEC-2000; 2000US-0750240.		QY	301	GGCGGACGGCTGAGGTGGCGCCGACGCGGTGCCAGAGTGGGGATCTCTGCTGGCGC	360
XX	27-DEC-1999; 99US-0472667.		DB	301	GGCGGACGGCTGAGGTGGCGCCGACGCGGTGCCAGAGTGGGGATCTCTGCTGGCGC	360
XX	(HAMM/) HAMMOND H K.		QY	361	CGTCTGGTGCAGGTGTTCCAGTGAAGCAGTTCGGTTCGGGCCAAGCTGAGAGCGCTGTAC	420
PA	(INSE/) INSEL P A.		DB	361	CGTCTGGTGCAGGTGTTCCAGTGAAGCAGTTCGGTTCGGGCCAAGCTGAGAGCGCTGTAC	420
PA	(PING/) PING P.		QY	421	CAGCGGTACTTCTCCAGATGAACCCAGAGCAGCCTGACGCTGCTGATGGGGTGTGGTG	480
PA	(POST/) POST S R.		DB	421	CAGCGGTACTTCTCCAGATGAACCCAGAGCAGCCTGACGCTGCTGATGGGGTGTGGTG	480
PA	(GAOM/) GAO M.		QY	481	CTGCTCACAGCGGTGCTGCTGGCTTTTCCACGCGCACCAGCGCCCTCAGCCCTGCCTAT	540
XX	Hammond HK, Insel PA, Ping P, Post SR, Gao M;		DB	481	CTGCTCACAGCGGTGCTGCTGGCTTTTCCACGCGCACCAGCGCCCTCAGCCCTGCCTAT	540
XX	WPI; 2002-690626/74.		QY	541	GTGGCACTGTTGGCTGTGCGCGCCCTGTTCTGTTGGGGCTCATGTGTGTGTAAACCGG	600
XX	P-PSDB; ABG32869.		DB	541	GTGGCACTGTTGGCTGTGCGCGCCCTGTTCTGTTGGGGCTCATGTGTGTGTAAACCGG	600
XX	Enhancing cardiac function in a mammal for treating heart disease such		QY	601	CATAGCTTCGCGCAGGACTCCATGTGGGTGGTGTAGTGTGTGTGGGCTGCTGGCGG	660
XX	as congestive heart failure, by delivering to the heart of the mammal a		DB	601	CATAGCTTCGCGCAGGACTCCATGTGGGTGGTGTAGTGTGTGTGGGCTGCTGGCGG	660
XX	vector comprising a gene encoding a beta-adrenergic signalling protein		QY	661	GCAGTGCAGGTGCGGGGCGCTCTCGCAGCAGACCCCGCAGCGCCCTCTGCGGGCTCTGG	720
XX	Claim 22; Page 42-44; 69pp; English.		DB	661	GCAGTGCAGGTGCGGGGCGCTCTCGCAGCAGACCCCGCAGCGCCCTCTGCGGGCTCTGG	720
XX	The invention relates to enhancing cardiac function in a mammal,		QY	721	TGCGCTGTGTTTGTGTACATGCGCTACAGCTCTCTCCCATCCGATCGGGCTGCC	780
XX	involves delivering a vector to the heart of the mammal, where the		DB	721	TGCGCTGTGTTTGTGTACATGCGCTACAGCTCTCTCCCATCCGATCGGGCTGCC	780
XX	vector comprises a gene encoding a beta-adrenergic signalling protein		QY	781	GTCTCTCAGCGGCTGGGCGCTCTCCACTTGTGATTTGATCTTGGCCCTGGCAACTTAACCGT	840
XX	(beta-ASP) e.g. adenylylase isoform 6 (AC-VI) operably linked to a		DB	781	GTCTCTCAGCGGCTGGGCGCTCTCCACTTGTGATTTGATCTTGGCCCTGGCAACTTAACCGT	840
XX	promoter. Generating a recombinant replication-defective viral particle		QY	841	GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGGCAATGTGCTGTCTCTGACCAAC	900
XX	involves introducing first and second plasmids into a replication-		DB	841	GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGGCAATGTGCTGTCTCTGACCAAC	900
XX	permissive mammalian cell expressing one or more adenovirus genes		QY	901	GTGATTGGGATGTGCAACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAAGAG	960
XX	confering replication competence, where the first plasmid comprises a		DB	901	GTGATTGGGATGTGCAACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAAGAG	960
XX	gene encoding a beta-ASP operably linked to a promoter and further		QY	961	ACCGCGGTTACATCCAGCGCCGCTCCACCTGTCAGTGCAGTGCAGAGGAGCGG	1020
XX	comprises a replication-defective human adenovirus genome, and the second		DB	961	ACCGCGGTTACATCCAGCGCCGCTCCACCTGTCAGTGCAGTGCAGAGGAGCGG	1020
XX	plasmid comprises a replication-competent human adenovirus genome and		QY	1021	CTGCTCTGTGGTATTGGCCCGCAGCAGTGGCATGAGATGAAAGAGACATCAACACA	1080
XX	further comprises an additional polynucleotide sequence making the second		DB	1021	CTGCTCTGTGGTATTGGCCCGCAGCAGTGGCATGAGATGAAAGAGACATCAACACA	1080
XX	plasmid too large to be encapsidated in an adenovirus particle, where		QY	1081	AAAAAGAGACATGATGTTTCCAAAGATCTTACATACAGAGCATGACATGTGAGCATC	1140
XX	rescue recombination takes place between the first plasmid and the second		DB	1081	AAAAAGAGACATGATGTTTCCAAAGATCTTACATACAGAGCATGACATGTGAGCATC	1140
XX	plasmid to generate a recombinant adenoviral genome comprising the gene		QY	1141	CTGTTTGCAGACATTCAGGCGCTTCCACGCTGGCATCCAGTGCAGTGCAGAGGAGCTG	1200
XX	encoding a beta-ASP but lacking one or more adenoviral replication genes,		DB	1141	CTGTTTGCAGACATTCAGGCGCTTCCACGCTGGCATCCAGTGCAGTGCAGAGGAGCTG	1200
XX	where the recombinant genome is sufficiently small to be encapsidated in		QY	1201	GTGATGACCCCTGAAATGAGCTCTTTTGGCCGGTTTGAACAGCTGGCTGCGGAGAAATCACTGC	1260
XX	an adenovirus particle, identifying successful recombinant viral vectors					
XX	in cell culture, and propagating a resulting recombinant viral particle					
XX	in replication-permissive mammalian cells expressing the missing					
XX	adenoviral replication genes to generate a recombinant replication-					
XX	defective viral particle. The method is useful for enhancing cardiac					
XX	function in a mammal, preferably human and is specifically useful for					
XX	treating heart diseases such as congestive heart failure (CHF).					
XX	The present sequence is a cDNA encoding human Adenylylase					
XX	isoform 6, AC-VI, a beta-ASP, used in the method of the invention.					
XX	Sequence 3552 BP; 686 A; 1037 C; 1068 G; 761 T; 0 other;					
SQ	Query Match	100.0%; Score 3552; DB 24; Length 3552;				
	Best Local Similarity	100.0%; Pred. No. 0;				
	Matches 3552; Conservative	0; Mismatches				
		0; Indels				
		0; Gaps				
QY	1	ATGTCATGTTTGTAGTGGCTCTCTGGTCCCTTAAAGTGGATGAACGGAAACAGCTGGGT	60			
DB	1	ATGTCATGTTTGTAGTGGCTCTCTGGTCCCTTAAAGTGGATGAACGGAAACAGCTGGGT	60			
QY	61	GAACGCAATGGCAGAGCGTTCCGCGCGCGGTGGCACTCGGCGAGGTGCTTCTGCACG	120			
DB	61	GAACGCAATGGCAGAGCGTTCCGCGCGCGGTGGCACTCGGCGAGGTGCTTCTGCACG	120			

1201 GTTCATGACCTGATGAGCTCTTTGCGCGGTTTGACAGCTGGCTGCGGAGAACTCACTGC 1260
1261 CTGAGGATCAAGATCTTTGGGAGACTGTTACTACTGTGTGTCAGGGTGC CGGAGCGCGG 1320
1261 CTGAGGATCAAGATCTTTGGGAGACTGTTACTACTGTGTGTCAGGGTGC CGGAGCGCGG 1320
1321 GCCGACCATGCCCACCTGCTGTGTGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1380
1321 GCCGACCATGCCCACCTGCTGTGTGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1380
1381 GTACGTGAGGTGACAGGTGTAATGTGAACATGCGGTGGGCATCCACAGCGGGCGGTG 1440
1381 GTACGTGAGGTGACAGGTGTAATGTGAACATGCGGTGGGCATCCACAGCGGGCGGTG 1440
1441 CACTGCGGCGTCTTGGCTTTCGGGAAATGGCAGTTTCGATGTGTGGTCCAAATGATGTGACC 1500
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1501 CTGGCCAAACCATGAGGAGCAGGAGCGCGGCTGGCCGATCCACATCACTCGGGCAACA 1560
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1621 TACCTCAAGGAGCAGCACATTCAGACTTTCCTCATCTGGGCGCCAGCCAGAGAAACGGAAA 1680
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1681 GAGGAGAGGCCATGCTGGCCAAAGCTGACGCGGACTCGGGCCAACTCCATGGAAGGGCTG 1740
1681 GAGGAGAGGCCATGCTGGCCAAAGCTGACGCGGACTCGGGCCAACTCCATGGAAGGGCTG 1740
1741 ATGCGCGGCTGGGTTCTGATCGTGCCTTCTCCCGGACCAAGGACTCCAGGACTTCGAGCTG 1800
1741 ATGCGCGGCTGGGTTCTGATCGTGCCTTCTCCCGGACCAAGGACTTCGAGCTG 1800
1801 CAGATGGGCAATGATGATTTCCAGCAAGAACACCGGGGACCCCAAGATGCCCTGAAACCT 1860
1801 CAGATGGGCAATGATGATTTCCAGCAAGAACACCGGGGACCCCAAGATGCCCTGAAACCT 1860
1861 GAGGATGAGGTGGATGAGTTCTGAGCGGTGCATCGATGCCCGCAGCACTGATCAGCTG 1920
1861 GAGGATGAGGTGGATGAGTTCTGAGCGGTGCATCGATGCCCGCAGCACTGATCAGCTG 1920
1921 CGGAAAGACCATGTGCGCGGTTTCTGCTCACCTTCCAGAGAGAGATCTTGAGAAGAAG 1980
1921 CGGAAAGACCATGTGCGCGGTTTCTGCTCACCTTCCAGAGAGAGATCTTGAGAAGAAG 1980
1981 TACTCCCGGAGGTGGATCCCGCTTCGGAGCCTACGTTGCGCTGTGCGCTGTGCTCTTC 2040
1981 TACTCCCGGAGGTGGATCCCGCTTCGGAGCCTACGTTGCGCTGTGCGCTGTGCTCTTC 2040
2041 TGCTTCATCTGCTTCATCAGCTTCTCAFTTCCACACACTCCACCTGATGCTGCGATC 2100
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2161 GGTTCCTGTTCCCTTAAGGCCCTGCAACGTGCTGCCGAGCATGTTGCGCTCAGGGCA 2220
2221 CATAGCACCGAGTTGGGATCTTTTCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
2221 CATAGCACCGAGTTGGGATCTTTTCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
2281 ATGTTCACTGTAAACACACCCCATACGAGCTGTGACGCGCGGATGCTGAAATTAACA 2340

2281 ATGTTCACTGTAAACACACCCCATACGAGCTGTGACGCGCGGATGCTGAAATTAACA 2340
2341 CCTGCTGACATCACTGCTGCGACCTGACAGAGCTCAATTAATCTCTCGGCTGATGCT 2400
2341 CCTGCTGACATCACTGCTGCGACCTGACAGAGCTCAATTAATCTCTCGGCTGATGCT 2400
2401 CCCCTGTGAGGGCACCATGCCACCTGACAGCTTCTCTGAGTACTTCTCATCGGGAACATG 2460
2401 CCCCTGTGAGGGCACCATGCCACCTGACAGCTTCTCTGAGTACTTCTCATCGGGAACATG 2460
2461 CTGCTGAGTCTTCTGGGCGAGCTCTGCTCTGCTGCAATCAGCAGCATCGGGAAGTTGGCC 2520
2461 CTGCTGAGTCTTCTGGGCGAGCTCTGCTCTGCTGCAATCAGCAGCATCGGGAAGTTGGCC 2520
2521 ATGATCTTGTCTTGGGGCTCATCTATTTGTGCTGCTTCTGCTGGGTCGCCAGCCACC 2580
2521 ATGATCTTGTCTTGGGGCTCATCTATTTGTGCTGCTTCTGCTGGGTCGCCAGCCACC 2580
2581 ATCTTTGACAACTATGACCTACTGCTTGGCGCTCCATGGCTTGGCTTCTTCCAATGAGACC 2640
2581 ATCTTTGACAACTATGACCTACTGCTTGGCGCTCCATGGCTTGGCTTCTTCCAATGAGACC 2640
2641 TTTGATGGGCTGAGCTGTCAGCTGCGAGGAGGGTGGCCCTCAATATATATGACCCCTGTG 2700
2641 TTTGATGGGCTGAGCTGTCAGCTGCGAGGAGGGTGGCCCTCAATATATATGACCCCTGTG 2700
2701 ATCTGCTGCTGTTTGGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
2701 ATCTGCTGCTGTTTGGGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2760
2761 CGCTAGACTTCTCTGGAACACTACAGGCAACAGGGGAGAGGAGAGATGAGGAGGCTA 2820
2761 CGCTAGACTTCTCTGGAACACTACAGGCAACAGGGGAGAGGAGAGATGAGGAGGCTA 2820
2821 CAGGATACAAACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
2821 CAGGATACAAACCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
2881 CTGGCCCGGAGCGCGCAATGATGAACTCTACTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
2881 CTGGCCCGGAGCGCGCAATGATGAACTCTACTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
2941 ATGTTTGGCTCCATTTGCCAACTTCTCTGAGTCTTCTGAGGCTGAGGAGGCAACAAATGAG 3000
2941 ATGTTTGGCTCCATTTGCCAACTTCTCTGAGTCTTCTGAGGCTGAGGAGGCAACAAATGAG 3000
3001 GGTGTGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060
3001 GGTGTGAGTGCCTGCGGCTGCTCAACGAGATCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3060
3061 GAGGAGCGGTTCCGGCAGCTGGAAGATCAAGAGTTCAGGAGTTCAGGAGTTCAGGAGTTCAGG 3120
3061 GAGGAGCGGTTCCGGCAGCTGGAAGATCAAGAGTTCAGGAGTTCAGGAGTTCAGGAGTTCAGG 3120
3121 TCAGGCTGGAACGGCAGCACCTACGATCAGGTGGGCGCTCCACATCACTGCTGCTGCTGCTG 3180
3121 TCAGGCTGGAACGGCAGCACCTACGATCAGGTGGGCGCTCCACATCACTGCTGCTGCTGCTG 3180
3181 GACTACGCCATGCGGCTCATGAGGAGATGAAGCAATCAATGAGCATCTCTTCAACAAAT 3240
3181 GACTACGCCATGCGGCTCATGAGGAGATGAAGCAATCAATGAGCATCTCTTCAACAAAT 3240
3241 TTCCAGATGAGATTTGGGCTGAACATGGGCGGCTGAGTGGGAGGAGTTCATCGGGGCTCGG 3300
3241 TTCCAGATGAGATTTGGGCTGAACATGGGCGGCTGAGTGGGAGGAGTTCATCGGGGCTCGG 3300
3301 AAGCCACAGTATGACATCTGGGGGAAACAGTGAATGCTCTAGTCTGCTGCTGCTGCTGCTGCTG 3360
3301 AAGCCACAGTATGACATCTGGGGGAAACAGTGAATGCTCTAGTCTGCTGCTGCTGCTGCTGCTG 3360
3361 GGGTCCCGGACCGAATCCAGGTGACCAAGGCTGTAACGAGGCTGCTAGCTGCTGCTGCTGCTGCTG 3420
3361 GGGTCCCGGACCGAATCCAGGTGACCAAGGCTGTAACGAGGCTGCTAGCTGCTGCTGCTGCTGCTG 3420

QY 3421 TACCAGCTGAGTGTGAGGGGTGCTCAAGTGAAGGGCAAGGGGAGATGACACCTAC 3480
 DB |||||||
 QY 3421 TACCAGCTGAGTGTGAGGGGTGCTCAAGTGAAGGGCAAGGGGAGATGACACCTAC 3480
 DB |||||||
 QY 3481 TTCTCTAATGGGGCCCGCCAGCAGTTAAACAGGGCCAGCCCAAAATTCAGTGAAGGACC 3540
 DB |||||||
 QY 3481 TTCTCTAATGGGGCCCGCCAGCAGTTAAACAGGGCCAGCCCAAAATTCAGTGAAGGACC 3540
 DB |||||||
 QY 3541 AAGTGGGCACT 3552
 DB |||||||
 QY 3541 AAGTGGGCACT 3552
 DB |||||||

RESULT 3

AAX00461

ID AAX00461 standard; cDNA; 4942 BP.

XX AC AAX00461;

XX 21-MAY-1999 (first entry)

XX Human type VI adenylyl cyclase cDNA.

XX Adenylyl cyclase type VI; human; hAC6; therapy; diagnosis; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 145..3651

XX /*tag= a

XX WO9901547-A1.

XX 14-JAN-1999.

XX 01-JUL-1998; 98WO-US13694.

XX 01-JUL-1997; 97US-0886550.

XX 01-JUL-1997; 97US-0070904.

XX (CORT-) COR THERAPEUTICS INC.

XX Tomlinson JA;

XX WPI; 1999-106049/09.

XX P-PSDB; AAW30599.

XX Newly isolated and purified human type VI adenylyl cyclase (hAC6)

XX polypeptide - useful for identifying potential therapeutic agents

XX that modulate hAC6 activity, and for the diagnosis of

XX hAC6-associated diseases and disorders

XX Claim 3; Fig 1A-I; 42pp; English.

XX This DNA sequence encodes human type VI adenylyl cyclase (hAC6, see

XX AAW30599) that is expressed mainly in the heart and brain. hAC6 has

XX a similar putative structure to other adenylyl cyclase isoforms

XX but, like type V, is distinguishable in that it has a larger

XX N-terminus and a relatively shorter C-terminus as it lacks the C2b

XX region. hAC6 cDNA was initially isolated from a human heart cDNA

XX library using an adenylyl cyclase PCR fragment as probe. It was

XX used to design primers that were used in a PCR-based RACE to obtain

XX the full-length cDNA sequence. The invention relates to the hAC6

XX gene, methods for the recombinant production of purified hAC6 and

XX the proteins made by these methods, antibodies against hAC6,

XX vectors, probes and host cells (especially HEK-293) transformed by

XX genes encoding polypeptides having hAC6 activity, along with

XX diagnostic and therapeutic uses for these various reagents. hAC6

XX can be used as a tool to screen for agonists and antagonists that

XX stimulate/inhibit hAC6. Such compounds have therapeutic utility

XX in treating diseases caused by aberrant activity of this enzyme,

XX and diseases whose symptoms can be ameliorated by stimulating or

CC inhibiting the activity of hAC6.

XX Sequence 4942 BP; 953 A; 1404 C; 1512 G; 1073 T; 0 other;

SQ

Query Match 99.8%; Score 3545.6; DB 20; Length 4942;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3548; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGTCAATGTTTGTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACAGCTGGGT 60

DB |||||||

QY 145 ATGTCAATGTTTGTAGTGGCTCTCTGCTCCCTAAAGTGGATGAACGGAACACAGCTGGGT 204

DB |||||||

QY 61 GAACGAATGGGCAGAAAGCTTCGCGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 120

DB |||||||

QY 205 GAACGAATGGGCAGAAAGCTTCGCGCGCGCTGGCACTCGGGCAGGTGGCTTCTGCACG 264

DB |||||||

QY 121 CCGCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCCCTCTGGGGCCCC 180

DB |||||||

QY 265 CCGCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCCCTCTGGGGCCCC 324

DB |||||||

QY 181 CCGCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCCCTCTGGGGCCCC 240

DB |||||||

QY 325 CCGCGCTATATGAGCTGCTCCGGGATGCAGAGCCACCCAGCCCCCTCTGGGGCCCC 384

DB |||||||

QY 241 GAGCTGGGGCTGCGGGCAGTGGCCCTTGGGCTTCAGAGATACCGAGGTGAACAACGACAGCG 300

DB |||||||

QY 385 GAGCTGGGGCTGCGGGCAGTGGCCCTTGGGCTTCAGAGATACCGAGGTGAACAACGACAGCG 444

DB |||||||

QY 301 GCGGGACCGCTGAGTGGGGCCCGGACGCGGTGCGCCAGAGTGGGGGATCTCTGTCGCGC 360

DB |||||||

QY 445 GCGGGACCGCTGAGTGGGGCCCGGACGCGGTGCGCCAGAGTGGGGGATCTCTGTCGCGC 504

DB |||||||

QY 361 CGTCTGGTGCAGGTGTTCCAGTGCAGAGCAGTTCCTGTCGGCCAAAGCTGGAGCGCTGTAC 420

DB |||||||

QY 505 CGTCTGGTGCAGGTGTTCCAGTGCAGAGCAGTTCCTGTCGGCCAAAGCTGGAGCAGCTGTAC 564

DB |||||||

QY 421 CAGCGGTACTTCTCCAGATGAACAGAGCAGCTGCAGCTGTGATGGCGGTGCTGGTG 480

DB |||||||

QY 565 CAGCGGTACTTCTCCAGATGAACAGAGCAGCTGCAGCTGTGATGGCGGTGCTGGTG 624

DB |||||||

QY 481 CTGCTCAGAGCGGTGCTGCTGGCTTCCAGCGCGCACCGCGCCCGCTCAGCGCTGCTAT 540

DB |||||||

QY 625 CTGCTCAGAGCGGTGCTGCTGGCTTCCAGCGCGCACCGCGCCCGCTCAGCGCTGCTAT 684

DB |||||||

QY 541 GTGGCACTGTTGGCTGTCGCGCGCCCTGTTCTGGTGGGCTCATGTGTGTGTAAACGG 600

DB |||||||

QY 685 GTGGCACTGTTGGCTGTCGCGCGCCCTGTTCTGGTGGGCTCATGTGTGTGTAAACGG 744

DB |||||||

QY 601 CATAGCTTCGCGCAGGACTCCATGTGGGTGGTGTAGTTACGTGTGTGTGGGCATCTGGCG 660

DB |||||||

QY 745 CATAGCTTCGCGCAGGACTCCATGTGGGTGGTGTAGTTACGTGTGTGTGGGCATCTGGCG 804

DB |||||||

QY 661 GCAGTGCAGGTGCGGGGGCGCTCTCGCAGCAGACCCCGGAGCCCTCTGGGGCGCTTGG 720

DB |||||||

QY 805 GCAGTGCAGGTGCGGGGGCGCTCTCGCAGCAGACCCCGGAGCCCTCTGGGGCGCTTGG 864

DB |||||||

QY 721 TGCCCTGTGTTCTTCTGTACATCGCTTACACGCTCTCTCCCATCGCATCGCGGTGCC 780

DB |||||||

QY 865 TGCCCTGTGTTCTTCTGTACATCGCTTACACGCTCTCTCCCATCGCATCGCGGTGCC 924

DB |||||||

QY 781 GTCTCTCAGGGGCGCTGGGGCTCTCCACCTTGCATTTGATCTTGGCCCTGGCAACTTAACCGT 840

DB |||||||

QY 925 GTCTCTCAGGGGCGCTGGGGCTCTCCACCTTGCATTTGATCTTGGCCCTGGCAACTTAACCGT 984

DB |||||||

QY 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCGCAATGTGCTGTCTCTCTGTCGACCAAC 900

DB |||||||

QY 985 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCGCAATGTGCTGTCTCTCTGTCGACCAAC 1044

DB |||||||

QY 901 GTCAATTTGGGATCTGCACACACTATCCAGCAGAGGTGCTCTCAGCGCCAGGGCTTTTCAGGAG 960

DB |||||||

QY 1045 GTCAATTTGGGATCTGCACACACTATCCAGCAGAGGTGCTCTCAGCGCCAGGGCTTTTCAGGAG 1104

DB |||||||

QY 961 ACCCGCGTTACATCCAGGCGCGGCTCCACCTGTCAGCATGAGAATCGGCAGAGGACGG 1020

DB |||||||

Db 1105 ACCCGGGTACATCCAGCCCGGCTCCACTGCGAGCATGAAATCGGAGCAGGCGG 1164
Qy 1021 CTGCTGCTGTCGGTATTCGCCAGACGTTGCCATCGGAGATGAAGAAGACATCAACACA 1080
Db 1165 CTGCTGCTGTCGGTATTCGCCAGACGTTGCCATCGGAGATGAAGAAGACATCAACACA 1224
Qy 1081 AAAAAAGAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATC 1140
Db 1225 AAAAAAGAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTCAGCATC 1284
Qy 1141 CTGTTTGCAGACATTCAGGGCTTCACAGCCTTGGAATCCAGTGCACTGCGCAGAGCTG 1200
Db 1285 CTGTTTGCAGACATTCAGGGCTTCACAGCCTTGGAATCCAGTGCACTGCGCAGAGCTG 1344
Qy 1201 GTCATGACCTGAATGAGCTCTTCCCGGTTTGAACAGCTGGCTGCGGAGAAATCACTGC 1260
Db 1345 GTCATGACCTGAATGAGCTCTTCCCGGTTTGAACAGCTGGCTGCGGAGAAATCACTGC 1404
Qy 1261 CTGAGGATCAAGATCTTGGGGACTGTTACTGTTGTCTCAGGGCTGCGGAGGCCCGG 1320
Db 1405 CTGAGGATCAAGATCTTGGGGACTGTTACTGTTGTCTCAGGGCTGCGGAGGCCCGG 1464
Qy 1321 GCCGACCATGCCACTGCTGTGTGAGATGCGGGGTAGACATGATTGAGGCCATCTCGCTG 1380
Db 1465 GCCGACCATGCCACTGCTGTGTGAGATGCGGGGTAGACATGATTGAGGCCATCTCGCTG 1524
Qy 1381 GTACGTGAGGTGACAGGTGGAATCTGAACATGCGCGTGGGCATCCACAGCGGGCGGTG 1440
Db 1525 GTACGTGAGGTGACAGGTGGAATCTGAACATGCGCGTGGGCATCCACAGCGGGCGGTG 1584
Qy 1441 CACTCGGGCGTCTTGGGCTTGCAGAAATGGCAGTTTCGATGTGTGTCGAAATGATGTACC 1500
Db 1585 CACTCGGGCGTCTTGGGCTTGCAGAAATGGCAGTTTCGATGTGTGTCGAAATGATGTACC 1644
Qy 1501 CTGGCCAAACCATGAGAGGACAGGAGCGCGGTGCGCGCATCCACATCTCGGGCAACA 1560
Db 1645 CTGGCCAAACCATGAGAGGACAGGAGCGCGGTGCGCGCATCCACATCTCGGGCAACA 1704
Qy 1561 CTGCAGTACCTGAAACGGGACTACAGGTGAGACGACGCGGTGGCGGCGCAACGG 1620
Db 1705 CTGCAGTACCTGAAACGGGACTACAGGTGAGACGACGCGGTGGCGGCGCAACGG 1764
Qy 1621 TACCTCAAGAGGACGACATTCAGACTTTCCTCATCTCGGGCGCGCAGCCAGAAACGGAAA 1680
Db 1765 TACCTCAAGAGGACGACATTCAGACTTTCCTCATCTCGGGCGCGCAGCCAGAAACGGAAA 1824
Qy 1681 GAGGAGAGGCGCATGCTGGCCAAAGCTGACGCGCACTCGGGCCAACTCCATGGAAGGGCTG 1740
Db 1825 GAGGAGAGGCGCATGCTGGCCAAAGCTGACGCGCACTCGGGCCAACTCCATGGAAGGGCTG 1884
Qy 1741 ATGCCGCGCTGGTTCTTGATCGTGCCTTCTCCGACCAAGGACTCCAGGCGCTTCCG 1800
Db 1885 ATGCCGCGCTGGTTCTTGATCGTGCCTTCTCCGACCAAGGACTCCAGGCGCTTCCG 1944
Qy 1801 CAGATGGGCAATTGATGATTCACAGCAAGACAAACCGGGCACCAAGATGCGCTGAACCT 1860
Db 1945 CAGATGGGCAATTGATGATTCACAGCAAGACAAACCGGGCACCAAGATGCGCTGAACCT 2004
Qy 1861 GAGGATGAGGTGATGATGTTCTGAGCCGTGTCATCGATGCGCGCAGCAATGATCAGCTG 1920
Db 2005 GAGGATGAGGTGATGATGTTCTGAGCCGTGTCATCGATGCGCGCAGCAATGATCAGCTG 2064
Qy 1921 CGGAAGGACCATGTCGCGCGTTCCTGCTCAGCTTCAGAGAGAGATCTTGAGAGAG 1980
Db 2065 CGGAAGGACCATGTCGCGCGTTCCTGCTCAGCTTCCTGCTCAGAGAGAGATCTTGAGAGAG 2124
Qy 1981 TACTCCCGAGGTGATGATCCCGCTTCGAGGCTACGTTGCGCTGCGCTGTTGTCCTTC 2040
Db 2125 TACTCCCGAGGTGATGATCCCGCTTCGAGGCTACGTTGCGCTGCGCTGTTGTCCTTC 2184
Qy 2041 TGCTTCATCTGCTTCATCAGCTTCCTCATCTTCCACATCTCCACCTGATGCTGGGATC 2100

Db 2185 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCACACTCCACCTGATGCTGGGATC 2244
Qy 2101 TATGCCAGCATCTTCTGCTGCTGCTAATACACGCTGATGCTGCTGCTGCTGCTGCTGCT 2160
Db 2245 TATGCCAGCATCTTCTGCTGCTGCTAATACACGCTGCTGCTGCTGCTGCTGCTGCTGCT 2304
Qy 2161 GTTCTCTGTTCCCTTAAGGCCCTGCAACGCTGCTGCCCGCAGCATTTGCTCCGCTCAGGGCA 2220
Db 2305 GTTCTCTGTTCCCTTAAGGCCCTGCAACGCTGCTGCCCGCAGCATTTGCTCCGCTCAGGGCA 2364
Qy 2221 CATAGACCGCAGTTGGCATCTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
Db 2365 CATAGACCGCAGTTGGCATCTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2424
Qy 2281 ATGTTCACTCTTAACCAACACCCCATACGAGCTGTCAGCCCGCATGCTGAAATTTAACA 2340
Db 2425 ATGTTCACTCTTAACCAACACCCCATACGAGCTGTCAGCCCGCATGCTGAAATTTAACA 2484
Qy 2341 CCTGCTGACATCACTGCTGCCACCTGCGAGCAGCTCAATTAATCTCTCTGGGCTGATGCT 2400
Db 2485 CCTGCTGACATCACTGCTGCCACCTGCGAGCAGCTCAATTAATCTCTCTGGGCTGATGCT 2544
Qy 2401 CCCCTGTGTGAGGGGACCATGCCCACTGCGAGCTTTCTCTGAGTACTTTCATCGGGAAATG 2460
Db 2545 CCCCTGTGTGAGGGGACCATGCCCACTGCGAGCTTTCTCTGAGTACTTTCATCGGGAAATG 2604
Qy 2461 CTGCTGAGTCTTCTGGCCAGCTGCTTCTCTGTCACATCAGCAGCATCGGGAAGTTGGCC 2520
Db 2605 CTGCTGAGTCTTCTGGCCAGCTGCTTCTCTGTCACATCAGCAGCATCGGGAAGTTGGCC 2664
Qy 2521 ATGATCTTGTCTTGGGGCTCATCTATTGCTGCTGCTTCTGCTGGGTCCCCAGCCACC 2580
Db 2665 ATGATCTTGTCTTGGGGCTCATCTATTGCTGCTGCTTCTGCTGGGTCCCCAGCCACC 2724
Qy 2591 ATCTTTGACAACTATGACTACTGCTGGCGCTCAATGCTGCTGCTTCTTCAATGAGACC 2640
Db 2725 ATCTTTGACAACTATGACTACTGCTGGCGCTCAATGCTGCTGCTTCTTCAATGAGACC 2784
Qy 2641 TTTGATGGGCTGAGCTGTCAGCTGCGAGGGGTGGCCCTCAATATATGACCCCTGTG 2700
Db 2785 TTTGATGGGCTGAGCTGTCAGCTGCGAGGGGTGGCCCTCAATATATGACCCCTGTG 2844
Qy 2701 ATTCTGCTGCTGTTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
Db 2845 ATTCTGCTGCTGTTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2904
Qy 2761 CGCTAGACTTCTCTGGAATACTACAGCAACAGGGGAGAGAGAGATGAGAGAGCTA 2820
Db 2905 CGCTAGACTTCTCTGGAATACTACAGCAACAGGGGAGAGAGAGATGAGAGAGCTA 2964
Qy 2821 CAGGCATACACCGGAGGCTGCTGCATTAACATCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
Db 2965 CAGGCATACACCGGAGGCTGCTGCATTAACATCTGCTGCTGCTGCTGCTGCTGCTGCT 3024
Qy 2881 CTGCGCGGAGCGCCCAATGATGAACTTACTATCATGCTGCTGCTGCTGCTGCTGCTGCT 2940
Db 3025 CTGCGCGGAGCGCCCAATGATGAACTTACTATCATGCTGCTGCTGCTGCTGCTGCTGCT 3084
Qy 2941 ATGTTTGCCTCCATGTCGCACTTCTGAGTTCATGTTGAGCTGAGGCAAAACATGAG 3000
Db 3085 ATGTTTGCCTCCATGTCGCACTTCTGAGTTCATGTTGAGCTGAGGCAAAACATGAG 3144
Qy 3001 GGTCTCGAGTGGCTGCGGCTGCTCAACGAGATCATCGTGTGCTGCTGCTGCTGCTGCTGCT 3060
Db 3145 GGTCTCGAGTGGCTGCGGCTGCTCAACGAGATCATCGTGTGCTGCTGCTGCTGCTGCTGCT 3204
Qy 3061 GAGGAGCGGTTTCCCGCAGCTGGAAGATCAAGACGATTGTTGAGCCTACATGCTGCTGCC 3120
Db 3205 GAGGAGCGGTTTCCCGCAGCTGGAAGATCAAGACGATTGTTGAGCCTACATGCTGCTGCC 3264
Qy 3121 TCAGGGCTGAACCGCAGCAGCTACGATCAGGTGGGCGCTCCCAATCACTGCTGCTGCT 3180
Db 3265 TCAGGGCTGAACCGCAGCAGCTACGATCAGGTGGGCGCTCCCAATCACTGCTGCTGCTGCT 3324

QY 3181 GACTACGCCATGGGCTCATGGAGCAGATGAAGCACAATCAATGAGCACTCTTCAACAAT 3240
 DB |||||
 QY 3325 GACTACGCCATGGGCTCATGGAGCAGATGAAGCACAATCAATGAGCACTCTTCAACAAT 3384
 DB |||||
 QY 3241 TTCAGATGAAGATTGGGCTGAACATGGGCCAGTCTGGCAGGTGTCTATGGGGCTCGG 3300
 DB |||||
 QY 3385 TTCAGATGAAGATTGGGCTGAACATGGGCCAGTCTGGCAGGTGTCTATGGGGCTCGG 3444
 DB |||||
 QY 3301 AAGCCAGATGACATCTGGGGGAACACATGTAATGTCTCTAGTCTATGACAGCAGC 3360
 DB |||||
 QY 3445 AAGCCAGATGACATCTGGGGGAACACATGTAATGTCTCTAGTCTATGACAGCAGC 3504
 DB |||||
 QY 3361 GGGGTCCCGACCGAATCCAGGTGACCAACGACCTGTACAGGTTCTAGCTGCCAAGGGC 3420
 DB |||||
 QY 3505 GGGGTCCCGACCGAATCCAGGTGACCAACGACCTGTACAGGTTCTAGCTGCCAAGGGC 3564
 DB |||||
 QY 3421 TACCAGCTGAGTGTCTGAGGGTGTCAAGGTGAAGGGCAAGGGGAGATGACCACTAC 3480
 DB |||||
 QY 3565 TACCAGCTGAGTGTCTGAGGGTGTCAAGGTGAAGGGCAAGGGGAGATGACCACTAC 3624
 DB |||||
 QY 3481 TTCTCTAATGGGGCCCCAGCAGTTTACAGGGCCAGCCCAAAATTCAGCTGAAGGACC 3540
 DB |||||
 QY 3625 TTCTCTAATGGGGCCCCAGCAGTTTACAGGGCCAGCCCAAAATTCAGCTGAAGGACC 3684
 DB |||||
 QY 3541 AAGGTGGGCACT 3552
 DB |||||
 QY 3685 AAGGTGGGCACT 3696
 DB |||||

RESULT 4

AAD08563
 ID AAD08563 standard; DNA; 3549 BP.
 AC AAD08563;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human cardiac adenylylase VI (ACVI) isoform #1 DNA.
 XX
 KW Human; cardiac; beta-adrenergic signalling protein; beta-ASP;
 KW myocardium; gene therapy; beta-adrenergic receptor; beta-AR;
 KW adenylylase; adenylylase; adenylylase; adenylylase;
 KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;
 KW cardiac adenylylase VI; ACVI isoform; beta-ASP transgene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 1..3504
 FT /*tag= a
 FT /product= "Human cardiac adenylylase VI isoform #1"
 FT /EC_number= "4.6.1.1"
 XX
 WO200148164-A2.
 XX
 PN 05-JUL-2001.
 XX
 PD 26-DEC-2000; 2000WO-US35411.
 XX
 PF 27-DEC-1999; 99US-0472667.
 XX
 PR (REGC) UNIV CALIFORNIA.
 XX
 PA Hammond HK, Gao M;
 XX
 PI WPI; 2001-418260/44.
 XX
 DR P-PSDB; AAE04310.
 XX
 PT Novel polynucleotide encoding a modified adenylylase polypeptide
 PT useful for enhancing cardiac function in mammalian hearts, and for
 PT treating heart disease, especially congestive heart failure -
 XX

Example 5; Page 122-129; 153pp; English.

PS The present invention relates to methods and compositions for enhancing
 XX cardiac function in mammalian hearts by inserting transgenes encoding
 CC beta-adrenergic signalling proteins (beta-ASP) which increase
 CC beta-adrenergic responsiveness within the myocardium using in vivo
 CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
 CC receptors (beta-AR), adenylylases (also referred to as adenylylase,
 CC adenylylase and adenylylase) and G-protein receptor kinase
 CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
 CC in mammalian hearts and for treating heart disease, especially
 CC congestive heart failure. The present DNA sequence encodes human
 CC cardiac adenylylase VI (ACVI) isoform which is used for generating
 CC a third beta-ASP transgene, used in the exemplification
 XX of the invention.
 SQ Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;
 Query Match 98.1%; Score 3484.8; DB 22; Length 3549;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 3517; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
 QY 1 ATGTCATGTTAGTGGCTCTCTGTCCTTAAAGTGAATGAACGAAACAGCCTGGGT 60
 DB 1 ATGTCATGTTAGTGGCTCTCTGTCCTTAAAGTGAATGAACGAAACAGCCTGGGT 60
 QY 61 GAACGCAATGGGCAGAAAGGTTTCGGCGCGCCGTCGCACTCGGCGAGTGGCTTCTGCACG 120
 DB 61 GAACGCAATGGGCAGAAAGGTTTCGGCGCGCCGTCGCACTCGGCGAGTGGCTTCTGCACG 120
 QY 121 CCCCCTATATGAGTGCCTTCGGGATGAGAGCCACCCAGCCCTCCCTGCGGGCCCC 180
 DB 121 CCCCCTATATGAGTGCCTTCGGGATGAGAGCCACCCAGCCCTCCCTGCGGGCCCC 180
 QY 181 CTTCTGGTCCCTTGGCAGATGACGCTTTCATCCGAGAGGGCGCCAGCAAGGCAAG 240
 DB 181 CTTCTGGTCCCTTGGCAGATGACGCTTTCATCCGAGAGGGCGCCAGCAAGGCAAG 240
 QY 241 GAGCTGGGCTGGCGCAGTGGCTTCGAGGATGAGAGTACAGAGTGAACAGCAGCG 300
 DB 241 GAGCTGGGCTGGCGCAGTGGCTTCGAGGATGAGAGTACAGAGTGAACAGCAGCG 300
 QY 301 GCGGACAGCTGAGTGGCGCCGAGCGGTGCCAGGAGTGGCGATCTCTCTGCGCGC 360
 DB 301 GCGGACAGCTGAGTGGCGCCGAGCGGTGCCAGGAGTGGCGATCTCTCTGCGCGC 360
 QY 361 CTTCTGGTGGAGTGTTCAGTGAAGCAGTTCGCTTGGCCAAAGCTGGAGCGCTGTAC 420
 DB 361 CTTCTGGTGGAGTGTTCAGTGAAGCAGTTCGCTTGGCCAAAGCTGGAGCGCTGTAC 420
 QY 421 CAGCGGTACTTCTCCAGATGACAGCAGCTGACGCTGCTGATGGCGGTGGTGTG 480
 DB 421 CAGCGGTACTTCTCCAGATGACAGCAGCTGACGCTGCTGATGGCGGTGGTGTG 480
 QY 481 CTGCTCACAGCGGTGTCTGCTTTCAGCGCGCACCCCGCCCGCTTCAGCCCTGCTAT 540
 DB 481 CTGCTCACAGCGGTGTCTGCTTTCAGCGCGCACCCCGCCCGCTTCAGCCCTGCTAT 540
 QY 541 GTGGCACTGTGGCTGTGGCGCGCTTTCGAGCGCGCTCATGGTGTGTGTAAACCG 600
 DB 541 GTGGCACTGTGGCTGTGGCGCGCTTTCGAGCGCGCTCATGGTGTGTGTAAACCG 600
 QY 601 CATAGCTTCGCCAGGACTCCATGTGGGTGGTGAATACCTGTGTGGCATCTCTGGCG 660
 DB 601 CATAGCTTCGCCAGGACTCCATGTGGGTGGTGAATACCTGTGTGGCATCTCTGGCG 660
 QY 661 GCAGTGCAGTGGGGGCGCTTCGCGAGCAGACCCCGCGAGCCCTCTCTGGCGCTCTGG 720
 DB 661 GCAGTGCAGTGGGGGCGCTTCGCGAGCAGACCCCGCGAGCCCTCTCTGGCGCTCTGG 720
 QY 721 TGCCCTGTGTTCTTTTCTATACATCGGCTTCTCCCATCGCATCGGGGTGCC 780
 DB 721 TGCCCTGTGTTCTTTTCTATACATCGGCTTCTCCCATCGCATCGGGGTGCC 780

781 GTCTCAGCGGCTGGGCTCTCCACCTTGGCAATTTGATCTTGGCCCTGGCAACTTAACCGT 840
781 GTCTCAGCGGCTGGGCTCTCCACCTTGGCAATTTGATCTTGGCCCTGGCAACTTAACCGT 840
841 GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCAATGTGCTGCTCTCTGCAACCAAC 900
841 GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCAATGTGCTGCTCTGCAACCAAC 900
901 GTCAATGGGATCTGCACACATATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
901 GTCAATGGGATCTGCACACATATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
961 ACCCGGGTTACATCAGCGCCGGCTCCACCTGCAAGATGAGAAATCGGAGAGGCGG 1020
961 ACCCGGAGTTACATCAGCGCCGGCTCCACCTGCAAGATGAGAAATCGGAGAGGCGG 1020
1021 CTGCTGCTGCTGGTATTGCCCCCAGCAGCTTGGCCATGGAGATGAAGAAGACATCAACACA 1080
1021 CTGCTGCTGCTGGTATTGCCCCCAGCAGCTTGGCCATGGAGATGAAGAAGACATCAACACA 1080
1081 AAAAAGAGACATGATGTTCCACAAGATCTACATACAGAAGCATGACAAATGTGAGCATC 1140
1081 AAAAAGAGAC --- ATGTTCCAAAGATCTACATACAGAAGCATGACAAATGTGAGCATC 1137
1141 CTGTTTGCAGACATGAGGGCTTCCACAGCCTGGCATCCAGTGCACCTGGCAGGAGGTG 1200
1138 CTGTTTGCAGACATGAGGGCTTCCACAGCCTGGCATCCAGTGCACCTGGCAGGAGGTG 1197
1201 GTCATGACCTGAATGAGCTCTTTGCGCGGTTTGACAGCTGGCTGGCGAGAAATCACTGC 1260
1198 GTCATGACCTGAATGAGCTCTTTGCGCGGTTTGACAGCTGGCTGGCGAGAAATCACTGC 1257
1261 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGACAGGCTGCGGAGGCCCGG 1320
1258 CTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGACAGGCTGCGGAGGCCCGG 1317
1321 GCCGCAATGCCATCTGTGTGTGGAGATGGGGGTAGACATGATTTGAGGCCATCTCGCTG 1380
1318 GCCGCAATGCCATCTGTGTGTGGAGATGGGGGTAGACATGATTTGAGGCCATCTCGCTG 1377
1381 GTACGTAGGTACAGGTGTGAATGTGAACATGCGGTGGGATCCACAGCGGGGCGGTG 1440
1378 GTACGTAGGTACAGGTGTGAATGTGAACATGCGGTGGGATCCACAGCGGGGCGGTG 1437
1441 CACTGCGGCTCTTGGCTTGGGAAATGCGCAGTTTCGATGTGTGTCGATGATGATGATGACC 1500
1438 CACTGCGGCTCTTGGCTTGGGAAATGCGCAGTTTCGATGTGTGTCGATGATGATGATGACC 1497
1501 CTGGCCAAACCATGAGGAGGAGGCGGCTGGCCGATCCACATCACTCGGGCAACA 1560
1498 CTGGCCAAACCATGAGGAGGAGGCGGCTGGCCGATCCACATCACTCGGGCAACA 1557
1561 CTGCAGTACCTGAACGGGACTACAGAGTGGAGCAGGCGGTGGTGGGAGCGCAACCGG 1620
1558 CTGCAGTACCTGAACGGGACTACAGAGTGGAGCAGGCGGTGGTGGGAGCGCAACCGG 1617
1621 TACCTCAAGGAGCAGCATTTGAGACTTTTCCTCATCTTGGGCGCAGCCAGAAACGGAAA 1680
1618 TACCTCAAGGAGCAGCATTTGAGACTTTTCCTCATCTTGGGCGCAGCCAGAAACGGAAA 1677
1681 GAGGAGAAAGGCCATCTGGCCAAAGCTGACGCGGATCTCGGGCCAACTCCATGGAAGGGCTG 1740
1678 GAGGAGAAAGGCCATCTGGCCAAAGCTGACGCGGATCTCGGGCCAACTCCATGGAAGGGCTG 1737
1741 ATGCGCGCTGGGTTCTGATCGTGCCTTTCTCCCGAACAGGATCTCAAGGCTTCCGC 1800
1738 ATGCGCGCTGGGTTCTGATCGTGCCTTTCTCCCGAACAGGATCTCAAGGCTTCCGC 1797
1801 CAGATGGGATGATGATTTCCAGCAAGACACCGGGGACCCAGATGCCCTGAAACCTT 1860
1798 CAGATGGGATGATGATTTCCAGCAAGACACCGGGGACCCAGATGCCCTGAAACCTT 1857

1861 GAGGATAGGTGGATGAGTTCTGAGCGGTGCCATCGATGCCCGCAGCATTTGATCAGCTG 1920
1858 GAGGATAGGTGGATGAGTTCTGAGCGGTGCCATCGATGCCCGCAGCATTTGATCAGCTG 1917
1921 CGGAAGGACCATGTGCGCGGGTTTCTGCTCACTTCCAGAGAGAGGATCTTGAGAAGAG 1980
1918 CGGAAGGACCATGTGCGCGGGTTTCTGCTCACTTCCAGAGAGAGGATTTTGAGAAGAG 1977
1981 TACTCCCGAAGGTGGATCCCGCTTCCGAGCTTACGTTGCTGCTGCTGCTGCTGCTGCT 2040
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2041 TGCTTCATCTGCTTTCATCCAGCTTCTCATCTTCCACACTCCACCTGATGCTGGGAT 2100
2038 TGCTTCATCTGCTTTCATCCAGCTTCTCATCTTCCACACTCCACCTGATGCTGGGAT 2097
2101 TATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
2098 TATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2157
2161 GGTCTCTGTTCCCTTAAGGCCCTGCAACGCTCTGCTCCGCGCAGCATTTGCTCAGGGCA 2220
2158 GGTCTCTGTTCCCTTAAGGCCCTGCAACGCTCTGCTCCGCGCAGCATTTGCTCAGGGCA 2217
2221 CATAGCAGCGAGTTGGCATCTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
2218 CATAGCAGCGAGTTGGCATCTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
2281 ATGTTCACTGTAAACCAACACCCCATACGAGCTGTGAGCGCGGATGCTGAATTTAACA 2340
2278 ATGTTCACTGTAAACCAACACCCCATACGAGCTGTGAGCGCGGATGCTGAATTTAACA 2337
2341 CCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
2338 CCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2397
2401 CCCCTGTGTAGGGCACCATGCCCTGACGCTTTCTGAGTACTTCTGAGTACTTCTGAGAACATG 2460
2398 CCCCTGTGTAGGGCACCATGCCCTGACGCTTTCTGAGTACTTCTGAGTACTTCTGAGAACATG 2457
2461 CTGCTGAGTCTTGTGGCCAGCTCTGCTTCTGCTGACATCAGCAGCATCGGGAAGTTGGCC 2520
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2698 ATCTGCTGCTGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2757
2761 CGCTTAGACTTCTCTGGAAACTACAGCAACAGGGGAGAGGAGAGATGGAGAGCTA 2820
2758 CGCTTAGACTTCTCTGGAAACTACAGCAACAGGGGAGAGAGAGAGATGGAGAGCTA 2817
2821 CAGGATCAACACCGGAGGCTGCTGATAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
2818 CAGGATCAACACCGGAGGCTGCTGATAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2877
2881 CTGCGCCGGAGCGCCCAATGATGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
2878 CTGCGCCGGAGCGCCCAATGATGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2937
2941 ATGTTTGCCTCCATTGCGCAACTTCTGAGTCTTCTATGTGAGCTGGAGGCAACAATGAG 3000

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Db 2938 ATGTTTCCCTCCATTGCAACTTCTCTGAGTTCTATGTGAGCTGGAGGCAACAATGAG 2997
Qy 3001 GGTGTGAGTCCCTGCGGCTGCTCAACGAGATCATCTGCTGACTTGTATGATATATCAGC 3060
Db 2998 GGTGCCAGTCCCTGCGGCTGCTCAACGAGATCATCTGCTGACTTGTATGATATATCAGC 3057
Qy 3061 GAGGAGCGGTTCCGGCAGCTGGAAGATCAAGACGATTGATGACCTACATGGCTGCC 3120
Db 3058 GAGGAGCGGTTCCGGCAGCTGGAAGATCAAGACGATTGATGACCTACATGGCTGCC 3117
Qy 3121 TCAGGCTGTAACGCCAGCACCCTACGATCAGGTGGGCGGCTCCCAATCATCTGCTGGCT 3180
Db 3118 TCAGGCTGTAACGCCAGCACCCTACGATCAGGTGGGCGGCTCCCAATCATCTGCTGGCT 3177
Qy 3181 GACTACGCCATGCGGCTCATGAGCAGATGAGCAGATCAATGAGCACTCTTCAACAAT 3240
Db 3178 GACTACGCCATGCGGCTCATGAGCAGATGAGCAGATCAATGAGCACTCTTCAACAAT 3237
Qy 3241 TTCCAGATGAAGATTGGGCTGAACATGGGCCAGTGTGTCAGTGTCTATGGGCTCGG 3300
Db 3238 TTCCAGATGAAGATTGGGCTGAACATGGGCCAGTGTGTCAGTGTCTATGGGCTCGG 3297
Qy 3301 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCTGTATGAGCAGCAG 3360
Db 3298 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCTGTATGAGCAGCAG 3357
Qy 3361 GGGTCCCGACCAATCCAGGTGACACAGCAGCTGTACAGAGTTTACGTGTCAGAGGC 3420
Db 3358 GGGTCCCGACCAATCCAGGTGACACAGCAGCTGTACAGAGTTTACGTGTCAGAGGC 3417
Qy 3421 TACCAGTGGAGTCTGAGGGGTGTCAGGTGAAGGCGAAGGGGAGATGACCACTAC 3480
Db 3418 TACCAGTGGAGTCTGAGGGGTGTCAGGTGAAGGCGAAGGGGAGATGACCACTAC 3477
Qy 3481 TTCTCAATGGGGCCCCAGCAGTTAAGGGCCCCAGCCCAAAATTCAGCTGAAGGACC 3540
Db 3478 TTCTCAATGGGGCCCCAGCAGTTAAGGGCCCCAGCCCAAAATTCAGCTGAAGGACC 3537
Qy 3541 AAGTGGGCACT 3552
Db 3538 AAGTGGGCACT 3549
```

RESULT 5

ABS54133
ID ABS54133 standard; cDNA; 3549 BP.

AC ABS54133;

XX 20-NOV-2002 (first entry)

XX Human cDNA encoding Adenylylase isoform 6, AC-VI.

XX Human; ss; gene; adenylylase isoform 6; AC-VI; CHF; gene therapy;
KW beta-adrenergic signalling protein; congestive heart failure; cardiac;
KW cardiac function; adenovirus vector; transgenic; gene therapy;
KW beta-adrenergic signalling protein; beta-ASP; heart disease.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..3504

FT /*tag= a

FT /EC number= "4.6.1.1"

FT /product= "Adenylylase isoform 6"

XX US2002103147-A1.

XX 01-AUG-2002.

XX 26-DEC-2000; 2000US-0750240.

XX

PR 27-DEC-1999; 99US-0472667.
XX (HAMM/) HAMMOND H K.
PA (INSE/) INSEL P A.
PA (PING/) PING P.
PA (POST/) POST S R.
PA (GAOM/) GAO M.
XX Hammond HK, Insel PA, Ping P, Post SR, Gao M;
PI WPI; 2002-690626/74.
XX P-PSDB; ABG32868.

DR Enhancing cardiac function in a mammal for treating heart disease such
XX as congestive heart failure, by delivering to the heart of the mammal a
XX vector comprising a gene encoding a beta-adrenergic signalling protein

XX Claim 75; Page 37-38; 69pp; English.

XX The invention relates to enhancing cardiac function in a mammal.
XX involves delivering a vector to the heart of the mammal, where the
XX vector comprises a gene encoding a beta-adrenergic signalling protein
XX (beta-ASP) e.g. adenylylase isoform 6 (AC-VI) operably linked to a
XX promoter. Generating a recombinant replication-defective viral particle
XX involves introducing first and second plasmids into a replication-
XX permissive mammalian cell expressing one or more adenovirus genes
XX conferring replication competence, where the first plasmid comprises a
XX gene encoding a beta-ASP operably linked to a promoter and further
XX comprises a replication-defective human adenovirus genome, and the second
XX plasmid comprises a replication-proficient human adenovirus genome and
XX further comprises an additional polynucleotide sequence making the second
XX plasmid too large to be encapsidated in an adenovirus particle, where
XX rescue recombination takes place between the first plasmid and the second
XX plasmid to generate a recombinant adenoviral genome comprising the gene
XX encoding a beta-ASP but lacking one or more adenoviral replication genes,
XX where the recombinant genome is sufficiently small to be encapsidated in
XX an adenovirus particle, identifying successful recombinant viral vectors
XX in cell culture, and propagating a resulting recombinant viral particle
XX in replication-permissive mammalian cells expressing the missing
XX adenoviral replication genes to generate a recombinant replication-
XX defective viral particle. The method is useful for enhancing cardiac
XX function in a mammal, preferably human and is specifically useful for
XX treating heart diseases such as congestive heart failure (CHF).
XX The present sequence is a cDNA encoding human Adenylylase
XX isoform 6, AC-VI, a beta-ASP, used in the method of the invention.

XX Sequence 3549 BP; 699 A; 1025 C; 1061 G; 764 T; 0 other;

XX Query Match 98.1%; Score 3484.8; DB 24; Length 3549;

XX Best Local Similarity 99.0%; Pred. No. 0;

XX Matches 3517; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTTATGTCGCTCTCTGTCCTTAAAGTGGATGAACGAAAAACAGCTGGGT 60

Db 1 ATGTCATGTTTATGTCGCTCTCTGTCCTTAAAGTGGATGAACGAAAAACAGCTGGGT 60

Qy 61 GAAGCAATGGGCAAGAGGTTCCGGCGCGCTGGGCACTCGGCGCAGGTGCTTCTGCACG 120

Db 61 GAAGCAATGGGCAAGAGGTTCCGGCGCGCTGGGCACTCGGCGCAGGTGCTTCTGCACG 120

Qy 121 CCCCGCTATATGAGTGCCTCCGGGATGAGAGCCACCCAGCCCCACCTCGGGGCCCC 180

Db 121 CCCCGCTATATGAGTGCCTCCGGGATGAGAGCCACCCAGCCCCACCTCGGGGCCCC 180

Qy 181 CTTGGTGGCTTGGCAGGATGACGCTTTCATCCGAGGGGGCGGCCAGCAAGGCAAG 240

Db 181 CTTGGTGGCTTGGCAGGATGACGCTTTCATCCGAGGGGGCGGCCAGCAAGGCAAG 240

Qy 241 GAGCTGGGCTGGGGCAGTGGGCTTTCAGGATACCGAGTGCACGACGACGCG 300

Db 241 GAGCTGGGCTGGGGCAGTGGGCTTTCAGGATACCGAGTGCACGACGACGCG 300

Qy	301	GGCGGAGCGCTGAGGTGGCGCCCGACGCGGTGCCCAAGAGTGGCGCGATCTCTGCTGGCGC	360
Db	301	GGCGGAGCGGTGAGGTGGCGCCCGACGCGGTGCCCAAGAGTGGCGCGATCTCTGCTGGCGC	360
Qy	361	CGTCTGCTGCAGGTGTTCCAGTCCGAACAGTTCCTGGTTCGGCCACAGCTGGAGCGCTGTAC	420
Db	361	CGTTTGGTGCAGGTGTTCCAGTCCGAACAGTTCCTGGTTCGGCCACAGCTGGAGCGCTGTAC	420
Qy	421	CAGCGGTACTTCTTCCAGATGAACCCAGAGCAGCCTGACGCTGCTGTGAATGGCGGTGCTGGTG	480
Db	421	CAGCGGTACTTTTTTCCAGATGAACCCAGAGCAGCCTGACGCTGCTGTGGTGGCGTGTGGTG	480
Qy	481	CTGCTCACAGCGGTGCTGTGGCTTTCACGCGCGACCCGCGCGCCCTCAGCCTGGCCTAT	540
Db	481	CTGCTCACAGCGGTGCTGTGGCTTTCCAAAGCGCGACCCGCGCGCCCTCAGCCTGGCCTAT	540
Qy	541	GTGGCACTGTTGGGCTGTGCGCGCGCCCTGTTTCGTGGGGCTCATGTGTGTGTAAACCGG	600
Db	541	GTGGCACTGTTGGGCTGTGCGCGCGCCCTGTTTCGTGGGGCTCATGTGTGTGTAAACCGG	600
Qy	601	CATAGCTTCGCGCCAGGACTCCATGTGGTGGTGAAGTTACGTGGTGTGGGCATCTGGCG	660
Db	601	CATAGCTTCGCGCCAGGACTCCATGTGGTGGTGAAGTTAAAGTGTGTGGGCATCTGGCG	660
Qy	661	GCAGTGCAGGTGGGGGGCTCTCGCAGCAGACCCGCGCAGCCCTCTGCGGGCTCTGG	720
Db	661	GCAGTGCAGGTGGGGGGCTTTTCGACAGCAGACCCGCGCGACCCCTCTGCGGGCTCTGG	720
Qy	721	TGCCCTGTGTTCTTGTCTACATCGCCTCAGCGCTCTCCCATCGCATGCGGGCTGCC	780
Db	721	TGCCCTGTGTTCTTGTATACATCGCATACGCTCTCTCCCATCGCATGCGGGCTGCC	780
Qy	781	GTCCTCAGCGGCTGGGCGCTCTCCACCTTGCAATTTGATCTTGGGCTGGCAACTTAACCGT	840
Db	781	GTCCTCAGCGGCTGGGCGCTCTCCACCTTGCAATTTGATCTTGGGCTGGCAACTTAACCGT	840
Qy	841	GGTGATGCCCTTCTCTGGAAAGCACTCGGTGCCAATGTGTGCTGTGTTCTCTGCAACAAC	900
Db	841	GGTGATGCCCTTCTCTGGAAAGCACTCGGTGCCAATGTGTGCTGTGTTCTCTGCAACAAC	900
Qy	901	GTCAATTCGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCGCTTTCAGGAG	960
Db	901	GTCAATTAGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCGCTTTCAGGAG	960
Qy	961	ACCGCGGTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAAATCGCAGCAGGAGCGG	1020
Db	961	ACCGCGAGTTACATCCAGGCGCGGCTCCACCTGCAGCATGAGAAATCGCAGCAGGAGCGG	1020
Qy	1021	CTGCTGTGTGCGTATTTGCCCGCAACGCTTGCATGAGATGAAGAAGACATCAACACA	1080
Db	1021	CTGCTGTGTGCGTATTTGCCCGCAACGCTTGCATGAGATGAAGAAGACATCAACACA	1080
Qy	1081	AAAAAAGACATGATGTTTCCCAAGATCTACATACAGAGCATGCAATGTGAGCATC	1140
Db	1081	AAAAAAGAGAC---ATGTTCCCAAGATCTACATACAGAGCATGCAATGTGAGCATC	1137
Qy	1141	CTGTTTTCAGACATTGAGGGCTTCCACAGCGCTGGCATCCAGTGCACTGCGCAGGAGCTG	1200
Db	1138	CTGTTTTCAGACATTGAGGGCTTCCACAGCGCTGGCATCCAGTGCACTGCGCAGGAGCTG	1197
Qy	1201	GTCATGACCTGAAATGAGCTCTTTTGGCCGGTTTGAACAGCTGGCTGCGGAGAAATCAATGC	1260
Db	1198	GTCATGACCTGAAATGAGCTCTTTTGGCCGGTTTGAACAGCTGGCTGCGGAGAAATCAATGC	1257
Qy	1261	CTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTGTGTACGGGCTGCGGAGGCGCGG	1320
Db	1258	CTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTGTGTACGGGCTGCGGAGGCGCGG	1317
Qy	1321	GCCGACCATGCCACTCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1380
Db	1318	GCCGACCATGCCACTCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG	1377
Qy	1381	GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTG	1440

Db	1378	GTACGTGAGGTGAACAGGTGTGAATGTGAACATACCGGTGGGCATCCACAGCGGCGCGTG	1437
Qy	1441	CACGTGCGCGTCCCTTGGCTTTCGGAAATGSCAGTTCGATGTGTGGTCCCAATGATGTGACC	1500
Db	1438	CACGTGCGCGTCCCTTGGCTTTCGGAAATGSCAGTTCGATGTGTGGTCCCAATGATGTGACC	1497
Qy	1501	CTGGCCAAACACATGGAGGAGGAGGCGGGCTGGCGCATCCACATCACTCGGGCAACA	1560
Db	1498	CTGGCCAAACACATGGAAAGCAGGAAGCGGGCTGGCGCATCCACATCACTCGGGCAACA	1557
Qy	1561	CTGCAGTACCTGAACGGGGACTACGAGGTGGAGCCAGGCGGTGGCGAGGCGCAACCGG	1620
Db	1558	CTGCAGTACCTGAACGGGGACTACGAAAGTGGAGCCAGGCGGTGGCGAAGCGCAACGGG	1617
Qy	1621	TACCTCAAGGAGCAGACATTTGAGACTTTCTCATCTCTGGGGCCAGGCAGAAACGGAAA	1680
Db	1618	TACCTCAAGGAGCAGACATTTGAGACTTTCTCATCTCTGGGGCCAGGCAGAAACGGAAA	1677
Qy	1681	GAGGAGAGGCCATGTCTGGCCAAAGCTGCACGGACCTCGGGCCAACTCCATGGAGAGGCTG	1740
Db	1678	GAGGAGAGAGCATGTCTGGCCAAAGCTGCACGGACCTCGGGCCAACTCCATGGAGAGGCTG	1737
Qy	1741	ATGCGCGCTGGGTTCTGTATCGTGGCTTCTCCGGACCAAGGACTCCAAAGGCTTCCCG	1800
Db	1738	ATGCGCGCATGGGTTCTGTATCGTGGCTTCTCCGGACCAAGGACTCCAAAGGCTTCCCG	1797
Qy	1801	CAGATGGGCATTGATGATTCACGAAAGACAACCGGGGCACCCAGATGCCCTGGAACCT	1860
Db	1798	CAGATGGGCATTGATGATTCACGAAAGACAACCGGGGCACCCAGATGCCCTGGAACCT	1857
Qy	1861	GAGATGAGGTGGATGAGTTTCTTGAGCGGTGCCATCGATGCCCGCAGCATTGATCAGCTG	1920
Db	1858	GAGGATGAGGTGGATGAGTTTCTTGAGCGGTGCCATCGATGCCCGCAGCATTGATCAGCTG	1917
Qy	1921	CGGAAGGACCATGTGGCGCGGTTTGTCTCACCTTCAGAGAGAGGATCTTGAGAGAAG	1980
Db	1918	CGGAAGGACCATGTGGCGCGGTTTGTCTCACCTTCAGAGAGAGGATTTTGAGAGAAG	1977
Qy	1981	TACTCCCGGAAGGTGATCCCGCTTCGGAGCCTACGTTGCCGTGCCCTGTGTGGTCTTC	2040
Db	1978	TACTCCCGGAAGGTGATCCCGCTTCGGAGCCTACGTTGCCGTGCCCTGTGTGGTCTTC	2037
Qy	2041	TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCACACTCCACCTCGATGCTTGGGATC	2100
Db	2038	TGCTTCATCTGCTTCATCCAGCTTCTAAATTTTCCACACTCCACCTCGATGCTTGGGAT	2097
Qy	2101	TATGCCAGCATCTTCTGTGCTGTCTTAATACCGTGCTGTATCTGTGCTGTACTCTGT	2160
Db	2098	TATGCCAGCATCTTCTGTGCTGTCTTAATACCGTGCTGTATCTGTGCTGTACTCTGT	2157
Qy	2161	GGTTCTCTGTTTCCCTAAGGCCCTGCAAGCTCTGTCCCGCAGAGATGTCGCTCACGGCA	2220
Db	2158	GGTTCTCTGTTTCCCTAAGGCCCTGCAAGCTCTGTCCCGCAGAGATGTCGCTCACGGCA	2217
Qy	2221	CATAGCACCGAGTTGGCATCTTTTCCGCTCTGTTGTGTACTTCTGCGCATGCGCAAC	2280
Db	2218	CATAGCACCGAGTTGGCATCTTTTCCGCTCTGTTGTGTACTTCTGCGCATGCGCAAC	2277
Qy	2281	ATGTTCACTGTAAACACACCCCATACGGAGCTGTGCAGCCCGGATGTGTAATTAAACA	2340
Db	2278	ATGTTCACTGTAAACACACCCCATACGGAGCTGTGCAGCCCGGATGTGTAATTAAACA	2337
Qy	2341	CCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTACTCTTGGGCTTGGATGT	2400
Db	2338	CCTGCTGACATCACTGCTGCCACCTGCAGCAGCTCAATTACTCTTGGGCTTGGATGT	2397
Qy	2401	CCCCTGTGTGAGGGCACCATGCCACCTGCAGCTTTCCTGAGTACTTCACTCGGAAACATG	2460
Db	2398	CCCCTGTGTGAGGGCACCATGCCACCTGCAGCTTTCCTGAGTACTTCACTCGGAAACATG	2457
Qy	2461	CTGCTGAGTCTCTTGGCCAGCTGTCTTCTCCACATCAGCAGCATCGGGAAGTTGGCC	2520

Db 2458 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGTCACATCAGCAGCATCGGGAAGTTGGCC 2517
Qy 2521 ATGATCTTTTGTCTGGGCTCATCTATTTGTGTGCTGTCTGTCTGGGTCCCCAGCCACC 2580
Db 2518 ATGATCTTTTGTCTGGGCTCATCTATTTGTGTGCTGTCTGTCTGGGTCCCCAGCCGCC 2577
Qy 2581 ATCTTTGACAACTATGACCTACTGCTTGGCTCCTCATGCTTGGCTTCTTCAATGAGACC 2640
Db 2578 ATCTTTGACAACTATGACCTACTGCTTGGCTCCTCATGCTTGGCTTCTTCAATGAGACC 2637
Qy 2641 TTTGATGGCTGGAGCTGTCAGCTGCAGGGAGGTCCTCAATATATGACCCCTGTG 2700
Db 2638 TTTGATGGCTGGAGCTGTCAGCTGCAGGGAGGTCCTCAATATATGACCCCTGTG 2697
Qy 2701 ATTCTGCTGTGTGTTGGCTGGCTGCTATCTGATGCTCAGCAGGTGGAGTCACTGCC 2760
Db 2698 ATTCTGCTGTGTGTTGGCTGGCTGCTATCTGATGCTCAGCAGGTGGAGTCACTGCC 2757
Qy 2761 CGCTAGACTTCTCTGGAACCTACAGGCAACAGGGAGAGAGGAGAGAGCTA 2820
Db 2758 CGCCTAACTTCTCTGGAACCTACAGGCAACAGGGAGAGAGAGAGAGAGCTA 2817
Qy 2821 CAGCATACACCGAGGCTGCTGCATACATCTGCGCCAGGAGCTGGCGGCCACTTC 2880
Db 2818 CAGCATACACCGAGGCTGCTGCATACATCTGCGCCAGGAGCTGGCGGCCACTTC 2877
Qy 2881 CTGGCCGGGAGCGCCGATGATGAATCTTACTATCAGTCTGTGATGTGTGGCTGTT 2940
Db 2878 CTGGCCGGGAGCGCCGATGATGAATCTTACTATCAGTCTGTGATGTGTGGCTGTT 2937
Qy 2941 ATGTTTGCCTCAATGTCACACTTCTGAGTTCTATGTGAGCTGGAGGCAAAACAATGAG 3000
Db 2938 ATGTTTGCCTCAATGTCACACTTCTGAGTTCTATGTGAGCTGGAGGCAAAACAATGAG 2997
Qy 3001 GGTGTGAGTGCCTGCGGCTGCTCAACAGATCATCTGATCTTGTATGATGATATCAGC 3060
Db 2998 GGTGTGAGTGCCTGCGGCTGCTCAACAGATCATCTGATCTTGTATGATGATATCAGC 3057
Qy 3061 GAGGAGCGGTTCGCGAGCTGGAAGATCAAGACGATTTGTAGCCTACATGAGCTGCTC 3120
Db 3058 GAGGAGCGGTTCGCGAGCTGGAAGATCAAGACGATTTGTAGCCTACATGAGCTGCTC 3117
Qy 3121 TCAGGCTGAAACGCGAGCCTACGATCAGTGGGCGCTGCCATCATCTGCTGCTGGCT 3180
Db 3118 TCAGGCTGAAACGCGAGCCTACGATCAGTGGGCGCTGCCATCATCTGCTGCTGGCT 3177
Qy 3181 GACTACGCCATGCGGCTCATGAGCAGATGAGCAGATCAATGAGCACTCTTCAACAAT 3240
Db 3178 GACTACGCCATGCGGCTCATGAGCAGATGAGCAGATCAATGAGCACTCTTCAACAAT 3237
Qy 3241 TTCCAGATGAAGATTGGCTGMAATGCGGCCAGTCTGTCGAGGTGTCTATCGGGGCTCGG 3300
Db 3238 TTCCAGATGAAGATTGGCTGMAATGCGGCCAGTCTGTCGAGGTGTCTATCGGGGCTCGG 3297
Qy 3301 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATCTCTAGTCTGTATGGAAGCAGC 3360
Db 3298 AAGCCACAGTATGACATCTGGGGGAACACAGTGAATCTCTAGTCTGTATGGAAGCAGC 3357
Qy 3361 GGGTCTCCGACCGAATCCAGGTGACCAAGCTGTACAGGTTCTAGTCTGCAAGGC 3420
Db 3358 GGGTCTCCGACCGAATCCAGGTGACCAAGCTGTACAGGTTCTAGTCTGCAAGGC 3417
Qy 3421 TACCAGCTGAGTGTCTGAGGGGTGCTCAAGTGAAGGGCAAGGGGAGATGACCACTAC 3480
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Qy 3481 TTCTCAATGGGGGCCCCAGCAGTTAAACAGGGCCCAAGCCCAAAATTCAGTGAAGGACC 3540
Db 3478 TTCTCAATGGGGGCCCCAGCAGTTAAACAGGGCCCAAGCCCAAAATTCAGTGAAGGACC 3537
Qy 3541 AAGTGGGCACT 3552
Db 3538 AAGTGGGCACT 3549

RESULT 6

AA080568
ID AAD08568 standard; cDNA; 3582 BP.

XX AAD08568;

AC AC
XX DT 04-SEP-2001 (first entry)

XX Human modified cardiac adenylcyclase VI (ACVI) isoform cDNA.

XX Human; cardiac; beta-adrenergic signalling protein; beta-ASP;
KW myocardiium; gene therapy; beta-adrenergic receptor; beta-AR;
KW adenylcyclase; adenylate cyclase; CAMP synthetase;
KW G-protein receptor kinase; GRK; heart disease; congestive heart failure;
KW cardiac adenylcyclase VI; ACVI isoform; beta-ASP transgene; ss.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX CDS 22..3525

XX FT /*tag= a

XX FT /product= "Human modified cardiac ACVI isoform"

XX WO200148164-A2.

XX PD 05-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US35411.

XX PR 27-DEC-1999; 99US-0472667.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Hammond HK, Gao M;

XX WPI; 2001-418260/44.

XX P-PSDB; AAE04312.

XX Novel polynucleotide encoding a modified adenylcyclase polypeptide
PT useful for enhancing cardiac function in mammalian hearts, and for
PT treating heart disease, especially congestive heart failure -

PS Claim 4; Page 143-150; 153pp; English.

XX The present invention relates to methods and compositions for enhancing
CC cardiac function in mammalian hearts by inserting transgenes encoding
CC beta-adrenergic signalling proteins (beta-ASP) which increase
CC beta-adrenergic responsiveness within the myocardium using in vivo
CC gene therapy. The beta-ASPs of the invention include beta-adrenergic
CC receptors (beta-AR), adenylcyclases (also referred as adenylcyclase,
CC adenylate cyclase and CAMP synthetase) and G-protein receptor kinase
CC (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function
CC in mammalian hearts and for treating heart disease, especially
CC congestive heart failure. The present cDNA sequence encodes human
CC modified cardiac adenylcyclase VI (ACVI) isoform which is used for
CC generating a beta-ASP transgene, used in the exemplification of the
CC invention.

XX Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;

Query Match 96.9%; Score 3443.2; DB 22; Length 3582;

Best Local Similarity 98.3%; Pred. No. 0;

Matches 3491; Conservative 0; Mismatches 58; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTTAGTGGCTCTCTGTCCTCAAGTGGATGAACGGAACAGCCTGGGT 60

Db 22 ATGTCATGTTTAGTGGCTCTCTGTCCTCAAGTGGATGAACGGAACAGCCTGGGT 81

Qy 61 GAACCAATGGGCAGAACGGTTCGCGGCCCTGGCACTCGGCGAGGTGCTTCGACG 120

Db 82 GAACGCAATGGGAGAGCGTTCCGGCGCGGTGGCACTCGGGAGGTGGCTTCTGACAG 141
Qy 121 CCCCGCTATATAGCTGCTCCGGATGACAGACCAACCAGCCCAACCTCTCGGGGCCCC 180
Db 142 CCCCGCTATATAGCTGCTCCGGATGACAGACCAACCAGCCCAACCTCTCGGGGCCCC 201
Qy 181 CTTCCGTGCTGCTGCGAGATGACGCTTTCATCCGAGGGGGGGCCAGGCAAGGGCAAG 240
Db 202 CTTCCGTGCTGCTGCGAGATGACGCTTTCATCCGAGGGGGGGCCAGGCAAGGGCAAG 261
Qy 241 GAGCTGGGGCTGCGGGAGTGGCCCTCGGGCTTCGAGGATACGAGGTGACAAACGACAGG 300
Db 262 GAGCTGGGGCTGCGGGAGTGGCCCTCGGGCTTCGAGGATACGAGGTGACAAACGACAGG 321
Qy 301 GCGGGACGCGCTGAGGTGGCGCCCGACGCGGTGCCAGAGTGGGCGATCTCTGCTGGCG 360
Db 322 GCGGGACGCGCTGAGGTGGCGCCCGACGCGGTGCCAGAGTGGGCGATCTCTGCTGGCG 381
Qy 361 CGTCTGGTGCAGGTGTTCCAGTGCAGAGAGTTCGGTTCGGGCCAAGTGGAGCGCTGTAC 420
Db 382 CGTCTGGTGCAGGTGTTCCAGTGCAGAGAGTTCGGTTCGGGCCAAGTGGAGCGCTGTAC 441
Qy 421 CAGCGGTACTTCTCCAGATGAACACAGACAGCCTGACGCTGCTGATGGCGGTGCTGGT 480
Db 442 CAGCGGTACTTCTCCAGATGAACACAGACAGCCTGACGCTGCTGATGGCGGTGCTGGT 501
Qy 481 CTGCTCACAGCGGTGCTGCTGGCTTTTCCAGCGCGCACCGCGCCCTCAGCGCTGCTAT 540
Db 502 CTGCTCACAGCGGTGCTGCTGGCTTTTCCAGCGCGCACCGCGCCCTCAGCGCTGCTAT 561
Qy 541 GTGGCACTGTTGGCTGTCGCGCGCTGTTCTGTTGTTGGGCTCATGGTGGTGTGAACCGG 600
Db 562 GTGGCACTGTTGGCTGTCGCGCGCTGTTCTGTTGGGCTCATGGTGGTGTGAACCGG 621
Qy 601 CATAGCTCCGCGAGACTCCATGTGGGTGGTGAATTAAGTGGTCTGGGCATCTGGCG 660
Db 622 CATAGCTCCGCGAGACTCCATGTGGGTGGTGAATTAAGTGGTCTGGGCATCTGGCG 681
Qy 661 GCAGTGCAGGTGCGGGCGCTCTCGCAGCAGACCGCGCAGCCCTCTGCGGGCTCTGG 720
Db 682 GCAGTGCAGGTGCGGGCGCTCTCGCAGCAGACCGCGCAGCCCTCTGCGGGCTCTGG 741
Qy 721 TGGCTGTGTTCTTTGTACATGCGCTACACGCTCTCTCCCATCCGATGCGGCTGCC 780
Db 742 TGGCTGTGTTCTTTGTACATGCGCTACACGCTCTCTCCCATCCGATGCGGCTGCC 801
Qy 781 GTCCCTCAGCGGCTGGGCTCTCCACCTTGCAATTTGATCTGGCTGGCACTTAACCGT 840
Db 802 GTCCCTCAGCGGCTGGGCTCTCCACCTTTGCAATTTGATCTGGCTGGCACTTAACCGT 861
Qy 841 GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCAATGTGCTGCTTCTCTGCAACCAAC 900
Db 862 GGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCAATGTGCTGCTTCTCTGCAACCAAC 921
Qy 901 GTCATGGCATCTGACACACTATCCAGCAGAGGTGTCTCAGCGCAGGCTTTCAGGAG 960
Db 922 GTCATGGCATCTGACACACTATCCAGCAGAGGTGTCTCAGCGCAGGCTTTCAGGAG 981
Qy 961 ACCCGGGTTACATCCAGGCCCGGCTCCACCTGCGAGCATGAGATCCGGCAGCAGAGCG 1020
Db 982 ACCCGGGTTACATCCAGGCCCGGCTCCACCTGCGAGCATGAGATCCGGCAGCAGAGCG 1041
Qy 1021 CTGCTGCTGCTGGTATTGGCCCGAGCAGCTGTGGCATGGAGATGAAGAAGACATCAACACA 1080
Db 1042 CTGCTGCTGCTGGTATTGGCCCGAGCAGCTGTGGCATGGAGATGAAGAAGACATCAACACA 1101
Qy 1081 AAAAAAGAGAATGATGTTTCCAAAGATCTTACATACAGAGCATGACAAATGTCAGCATC 1140
Db 1102 AAAAAAGAGAATGATGTTTCCAAAGATCTTACATACAGAGCATGACAAATGTCAGCATC 1161
Qy 1141 CTGTTTGCAGACATTTAGGGCTTCCACCGCTGGCATCCAGTGCATGCGCAGAGCTG 1200
Db 1162 CTGTTTGCAGACATTTAGGGCTTCCACCGCTGGCATCCAGTGCATGCGCAGAGCTG 1221

Qy 1201 GTCATGACCTGAATGAGCTCTTTGCCCGGTTTGAACAAGCTGGCTGCGGAGAACTCACTGC 1260
Db 1222 GTCATGACCTTGAATGAGCTCTTTGCCCGGTTTGAACAAGCTGGCTGCGGAGAACTCACTGT 1281
Qy 1261 CTGAGGATCAAGATCTTTGGGGGACTGTCTACTGTGTGTCAAGGGCTGCGGAGGCCCGG 1320
Db 1282 CTGAGGATCAAGATCTTTAGGAGACTGTCTACTGTGTGTCAAGGGCTGCGGAGGCCCGG 1341
Qy 1321 GCGGACCATGCCACTGTGTGTGAGATGGGGGTAGACATGATTTGAGGCACTCTCGCTG 1380
Db 1342 GCAGATCAGGCCACTGTGTGTGAGATGGGGGTAGACATGATTCGAAGCCATCTCGCTG 1401
Qy 1381 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCTG 1440
Db 1402 GTGCGTAGGTTAAACAGGTGTGAACGTGAACATGCGTGTGGGCATCCACAGCGGACGTGTG 1461
Qy 1441 CACTCGCGGCTCTTTGGCTTGGGAAATGGCAGATTCGATGTGTGTGTCGAATGTGACC 1500
Db 1462 CATTCGCGGCTCTTTGGCTTACGGAAATGGCAGATTTGATGTGTGTGTCGAACGATGTGACC 1521
Qy 1501 CTGGCCAAACACATGAGGAGGAGGCGGCGTGGCCGATCCACATCACTCGGGCAACA 1560
Db 1522 CTGGCTAACACATGAGGAGGCGGCGC---GGCGGCGCATCCACATCACTCGGGCTACA 1578
Qy 1561 CTGCAGTACCTGAACGGGGACTACGAGGTGGAGCCAGGCCGCTGGTGGCGAGCGCAACCG 1620
Db 1579 CTGCAGTACTTTGAACGGGGACTATGAGGTGGAGCCAGGCCGCTGGTGGTGAACGCAATGG 1638
Qy 1621 TACCTCAAGGAGCAGACATTTGAGACTTTCCTCATCTCTGGGGCCAGCCAGAAACGGAAA 1680
Db 1639 TACCTCAAGGAGCAGTGCATTTGAGACCTTTCCTCATCTCTGGCGCCAGCCAAAAACGGAAA 1698
Qy 1681 GAGGAGAGGCCATCTGGCCCAAGCTGCAGCGGACTCGGGCCCACTCCATCGAAGGGCTG 1740
Db 1699 GAGGAGAGGCCATCTGGCCCAAGCTTCAGCGGACACGGGCCCACTCCATCGAAGGACTG 1758
Qy 1741 ATGCCGCGCTGGGTTCTGTGATCTGTCCTTCTCCCGGACCAAGGACTCCCAAGGCCCTTCGCG 1800
Db 1759 ATGCCGCGCTGGGTTCTGTGACCGTGTCTCTCCCGGACCAAGGACTCTTAAGGCATTCGCG 1818
Qy 1801 CAGATGGGCATTTGATGATTCAGCAAAAGACAACCGGGGCAACCAAGATGCCCTGAAACCT 1860
Db 1819 CAGATGGGCATTTGATGATTTAGCAAAAGACAACCGGGGTGCGCAAGATGCTCTGAAACCT 1878
Qy 1861 GAGATGAGGTGGATGATCTGAGCGGTGCGCATCGATGCCCGCAGCATTTGATCAGCTG 1920
Db 1879 GAAATGAGGTGGATGATCTCTGGCGGAGGCCATCGATGCCCGCAGCATTTGATCAGCTG 1938
Qy 1921 CGGAAGGACCATGTGCGCGGTTTCTGCTCACCTTCCAGAGAGAGGATCTTTGAGAAAGAG 1980
Db 1939 CGGAAGGACCATGTGCGCGGTTTCTGCTCACCTTCCAGAGAGAGGATCTTTGAGAAAGAG 1998
Qy 1981 TACTCCCGGAAAGTGGATCCCGCTTGGAGCCCTACGTTGCTGTGCTGTGCTGTTC 2040
Db 1999 TACTCCCGGAAAGTGGATCCCGCTTGGAGCCCTACGTTGCTGTGCTGTGCTGTTC 2058
Qy 2041 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCACACATCCACCTCGATGCTGGGATC 2100
Db 2059 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCACACATCCACCTCGATGCTGGGATC 2118
Qy 2101 TATGCCAGCATCTTCTGCTGCTGCTAATCACCGTGTGATCTGTGCTGTGTACTCTCTGT 2160
Db 2119 TATGCCAGCATCTTCTGCTGCTGCTAATCACCGTGTGATCTGTGCTGTGTACTCTCTGT 2178
Qy 2161 GGTTCCTGTTTCCCTAAGGCCCTCGAAGCTGTGTCGCGCAGCATTTGTCGCTCAGCGCA 2220
Db 2179 GGTTCCTGTTTCCCTAAGGCCCTCGAAGCTGTGTCGCGCAGCATTTGTCGCTCAGCGCA 2238
Qy 2221 CATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTGTGTTTACTTTCTGCCCATTCGCAAC 2280
Db 2239 CATAGCACCGCAGTTGGCATCTTTTCCGTCCTGCTGTGTTTACTTTCTGCCCATTCGCAAC 2298

conferring replication competence, where the first plasmid comprises a
 gene encoding a beta-ASP operably linked to a promoter and further
 comprises a replication-defective human adenovirus genome, and the second
 plasmid comprises a replication-competent human adenovirus genome and
 further comprises an additional polynucleotide sequence making the second
 plasmid too large to be encapsidated in an adenovirus particle, where
 rescue recombination takes place between the first plasmid and the second
 plasmid to generate a recombinant adenoviral genome comprising the gene
 encoding a beta-ASP but lacking one or more adenoviral replication genes,
 where the recombinant genome is sufficiently small to be encapsidated in
 an adenovirus particle, identifying successful recombinant viral vectors
 in cell culture, and propagating a resulting recombinant viral particle
 in replication-permissive mammalian cells expressing the missing
 adenoviral replication genes to generate a recombinant replication-
 defective viral particle. The method is useful for enhancing cardiac
 function in a mammal, preferably human and is specifically useful for
 treating heart diseases such as congestive heart failure (CHF).
 The present sequence is a chimeric cDNA encoding human/mouse
 Adenyllylase isoform 6, AC-VI, a beta-ASP, used in the method of the
 invention.

Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;
 SQ

Sequence 3582 BP; 703 A; 1036 C; 1067 G; 776 T; 0 other;

Query Match 96.9%; Score 3443.2; DB 24; Length 3582;

Best Local Similarity 98.3%; Pred. No. 0;

2000 Local Similarity 50.5%; ID: NO. 0;
Matches 3491; Conservative 0; Mismatches 58; Indels 3; Gaps 1;

Qy	1	ATGTCATGTTTAGTGGCCCTCTGTGTCCTTAAAGTGGATGAACGGAAAAACAGCTGGGT	60
Db	22	ATGTCATGTTTAGTGGCCCTCTGTGTCCTTAAAGTGGATGAACGGAAAAACAGCTGGGT	81
Qy	61	GAACGCAATGGGCAGAAAGGTTTCGGGCGCGTGGCACTCGGCAGGTGGCTTCTGCACG	120
Db	82	GAACGCAATGGGCAGAAAGGTTTCGGGCGCGTGGCACTCGGCAGGTGGCTTCTGCACG	141
Qy	121	CCCGCTATATGAGTGGCTTCGCGGATGCAGAGCCACCCAGCCCCACCTCGGGGCCCC	180
Db	142	CCCGCTATATGAGTGGCTTCGCGGATGCAGAGCCACCCAGCCCCACCTCGGGGCCCC	201
Qy	181	CCTCGGTGCCCTGGCAGAGATGACCCCTTTCATTCGGAGGGCGGCCACGAGGAAGGCAAG	240
Db	202	CCTCGGTGCCCTGGCAGAGATGACCCCTTTCATTCGGAGGGCGGCCACGAGGAAGGCAAG	261
Qy	241	GAGCTCGGGCTGCGGSCAGTGSCCTCGGGCTTCAGAGGATACCGAGGTGACAAACAGACGG	300
Db	262	GAGCTCGGGCTGCGGSCAGTGSCCTCGGGCTTCAGAGGATACCGAGGTGACAAACAGACGG	321
Qy	301	GGCGGACGGCTGAGGTGCGGCCCGACGCGGTGCCAGGAGTGGGCGCATCTGCTGGCGC	360
Db	322	GGCGGACGGCTGAGGTGCGGCCCGACGCGGTGCCAGGAGTGGGCGCATCTGCTGGCGC	381
Qy	361	CGTCTGCTCAGGTGTTCCAGTTCGAAGCAGATTTCGTTTCGGCCAAAGCTGGAGCCCTGTAC	420
Db	382	CGTCTGCTCAGGTGTTCCAGTTCGAAGCAGATTTCGTTTCGGCCAAAGCTGGAGCCCTGTAC	441
Qy	421	CAGCGGTACTTCTTCAGATGAACACAGACAGCCTGACGCTGCTGATGGCGGTGCTGGTG	480
Db	442	CAGCGGTACTTCTTCAGATGAACACAGACAGCCTGACGCTGCTGATGGCGGTGCTGGTG	501
Qy	481	CTGCTCACAGCGGTGCTGTGGCTTTCCACGCGCACCCCGCCCGCTTCAGCCTGCCTAT	540
Db	502	CTGCTCACAGCGGTGCTGTGGCTTTCCACGCGCACCCCGCCCGCTTCAGCCTGCCTAT	561
Qy	541	GTGGCACTGTTGGCTGTGGCCCGCCCTGTTGTTGTTGGGCTCATGTGGTGTGTAAACGG	600
Db	562	GTGGCACTGTTGGCTGTGGCCCGCCCTGTTGTTGTTGGGCTCATGTGGTGTGTAAACGG	621
Qy	601	CATAGCTTCGGCAGGACTCCATGTGGGTGTGAGTTACGTGGGTCTGGGCACTCTGGCG	660
Db	622	CATAGCTTCGGCAGGACTCCATGTGGGTGTGAGTTACGTGGGTCTGGGCACTCTGGCG	681
Qy	661	GCAGTCCAGGTTCGGGGGCGCTCTCGCAGACAGCCCGCGCAGCCCTCTCGGGGCTCTGG	720

Qy	1801	CAGATGGGCATTTGATGATTCCAGCAAAAGACAACCGGGGCA	CCCCAAGATGCCCTGAACCCCT	1860
Db	1819	CAGATGGGCATTTGATGATTCTAGCAAAAGACAACCGGGGTGCC	CCCAAGATGCTCTGAACCCCT	1878
Qy	1861	GAGGATGAGGTGGATGATGTTCTTGAGCGGTGCCATCGATCGCCCGCAGCATTTGATCAGCTG		1920
Db	1879	GAAGATGAGGTGGATGATGTTCTTGGGCCGAGCCATCGATGCCGACAGCATTTGATCAGCTG		1938
Qy	1921	CGGAAAGACCATGTGCGCCGGTTTCTGCTCACCTTCCAGAGAGAGGATCTTGAGAGAAG		1980
Db	1939	CGGAAAGACCATGTGCGCCGGTTTCTGCTCACCTTCCAGAGAGAGGATCTTGAGAGAG		1998
Qy	1981	TACTCCCGGAAGTGGATCCCGCTTCGAGCCTTACGTTGCCTGTGCCCTGTTGGTCTTC		2040
Db	1999	TACTCCCGGAAGTGGATCCCGCTTCGAGCCTTACGTTGCCTGTGCCCTGTTGGTCTTC		2058
Qy	2041	TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACTCCACCTTGATGCTTGGGATC		2100
Db	2059	TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCCACTCCACCTTGATGCTTGGGATC		2118
Qy	2101	TATGCCAGCATCTTCTGCTGCTGAATCACCGTGTGATCTGTGCTGTGTAATCTTCTGT		2160
Db	2119	TATGCCAGCATCTTCTGCTGCTGAATCACCGTGTGATCTGTGCTGTGTAATCTTCTGT		2178
Qy	2161	GGTTCTCTGTTCCCTAAGGGCCCTGCACAGCTGTGCCGAGCATTTGCCCTCACGGGCA		2220
Db	2179	GGTTCTCTGTTCCCTAAGGGCCCTGCACAGCTGTGCCGAGCATTTGCCCTCACGGGCA		2238
Qy	2221	CATAGCACCGGAGTGGATCTTTTTCGCTGCTGTGTGTGTTACTTCTGCGATGCTGTAATCT		2280
Db	2239	CATAGCACCGGAGTGGATCTTTTTCGCTGCTGTGTGTGTTACTTCTGCGATGCTGTAATCT		2298
Qy	2281	ATGTTACCTGTAAACACACCCCATACGGAGCTGTGCAGCCGAGTCTGAATTTAAACA		2340
Db	2299	ATGTTACCTGTAAACACACCCCATACGGAGCTGTGCAGCCGAGTCTGAATTTAAACA		2358
Qy	2341	CCTGCTGACATCACTGCTGCTGCCACTGCAGCAGCTCAATTAATCTCTCGGSCCTTGGATGCT		2400
Db	2359	CCTGCTGACATCACTGCTGCTGCCACTGCAGCAGCTCAATTAATCTCTCGGSCCTTGGATGCT		2418
Qy	2401	CCCCTGTGTAGGGGCAACATGCCCACTGCAGCTTTTCTGAGTACTTTCATCGGGAAACATG		2460
Db	2419	CCCCTGTGTAGGGGCAACATGCCCACTGCAGCTTTTCTGAGTACTTTCATCGGGAAACATG		2478
Qy	2461	CTGCTGAGTCTCTTGGCCAGCTCTGCTTCTGACATCAGCAGCATCGGGAGTTGGCC		2520
Db	2479	CTGCTGAGTCTCTTGGCCAGCTCTGCTTCTGACATCAGCAGCATCGGGAGTTGGCC		2538
Qy	2521	ATGATCTTTGTCTTGGGGCTCATCTATTGGTGTGCTTCTGCTGGGTCCCCCAGCCACC		2580
Db	2539	ATGATCTTTGTCTTGGGGCTCATCTATTGGTGTGCTTCTGCTGGGTCCCCCAGCCACC		2598
Qy	2581	ATCTTTGACAACTATGACCTACTGCTTGGCGTCCANGCTTGGCTTCTTCCAATGAGACC		2640
Db	2599	ATCTTTGACAACTATGACCTACTGCTTGGCGTCCANGCTTGGCTTCTTCCAATGAGACC		2658
Qy	2641	TTTGATGGGCTGGACTGTGACGCTGCAGGAGGGGTGGCCCTCAAAATATGACCCCTGTG		2700
Db	2659	TTTGATGGGCTGGACTGTGACGCTGCAGGAGGGGTGGCCCTCAAAATATGACCCCTGTG		2718
Qy	2701	ATTCCTGCTGTTTGGCTGGCGCTCTATCTGATGCTCAGCAGGTGGAGTGCAGCTGCC		2760
Db	2719	ATTCCTGCTGTTTGGCTGGCGCTCTATCTGATGCTCAGCAGGTGGAGTGCAGCTGCC		2778
Qy	2761	CGCCTAGACTTCTCTCTGGAACCTACAGGCAACAGGGGAGAGGAGATGAGGAGCTA		2820
Db	2779	CGCCTAGACTTCTCTCTGGAACCTACAGGCAACAGGGGAGAGGAGATGAGGAGCTA		2838
Qy	2821	CAGGCATCAACCGGAGGCTGCTGCATAACATTTCTGCCAAGNACGTGGCGGCCACTTC		2880
Db	2839	CAGGCATCAACCGGAGGCTGCTGCATAACATTTCTGCCAAGNACGTGGCGGCCACTTC		2898

Qy	2881	CTGGCCGGGAGCGCCGCAATGATGAACCTTACTATCATCAGTCGTTGAGTGTGTGGCTGTT	2944
Db	2899	CTGGCCGGGAGCGCCGCAATGATGAACCTTACTATCATCAGTCGTTGAGTGTGTGGCTGTT	2958
Qy	2941	ATGTTTGGCTCCATGTCGAACCTTCTCTGAGTTCTATGTGGAGCTGCGAGCAACAATGAG	3000
Db	2959	ATGTTTGGCTCCATGTCGAACCTTCTCTGAGTTCTATGTGGAGCTGCGAGCAACAATGAG	3018
Qy	3001	GGTGTTCAGTGCCTGGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC	3060
Db	3019	GGTGTTCAGTGCCTGGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGC	3078
Qy	3061	GAGAGCGGTTCCGGCAGCTGGAAAAAGATCAAGACGATTGGTTAGCACTTATATGGCTGCC	3120
Db	3079	GAGAGCGGTTCCGGCAGCTGGAAAAAGATCAAGACGATTGGTTAGCACTTATATGGCTGCC	3138
Qy	3121	TCAGGGCTGAAGCCAGCACCTTACGATCAGGTGGGCGGCTCCCAACATCACTGCGCCTGGCT	3180
Db	3139	TCAGGGCTGAAGCCAGCACCTTACGATCAGGTGGGCGGCTCCCAACATCACTGCGCCTGGCT	3198
Qy	3181	GACTACGCCATGCGGCTCATGGAGCAGATGAAGCAACATCAATGAGCACTCTTTCAACAAT	3240
Db	3199	GACTACGCCATGCGGCTCATGGAGCAGATGAAGCAACATCAATGAGCACTCTTTCAACAAT	3258
Qy	3241	TTCCAGATGAAGATTGGGCTGAACATGGGCCCCAGTCGTGGCAGGTGTCTATCGGGGCTCGG	3300
Db	3259	TTCCAGATGAAGATTGGGCTGAACATGGGCCCCAGTCGTGGCAGGTGTCTATCGGGGCTCGG	3318
Qy	3301	AAGCCACAGTATGACATCTCGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCAGC	3360
Db	3319	AAGCCACAGTATGACATCTCGGGGGAACACAGTGAATGTCTCTAGTCGTATGGACAGCAGC	3378
Qy	3361	GGGTCCCCGACCGAATCCAGGTGACACGCGACTGTACCAGGTTCCTAGCTGCAAGGGC	3420
Db	3379	GGGTCCCCGACCGAATCCAGGTGACACGCGACTGTACCAGGTTCCTAGCTGCAAGGGC	3438
Qy	3421	TACCAGCTCGAGTGTCCAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTTAC	3480
Db	3439	TACCAGCTCGAGTGTCCAGGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCACTTAC	3498
Qy	3481	TTCTCTAATGGGGGCCCCAGCAGTTAACAGGGCCCCAGCCCAAAATTCAGCTGAAGGGACC	3540
Db	3499	TTCTCTAATGGGGGCCCCAGCAGTTAACAGGGCCCCAGCCCAAAATTCAGCTGAAGGGACC	3558
Qy	3541	AAGTGGGCACT 3552	
Db	3559	AAGTGGGCACT 3570	
RESULT 8			
ID	AAQ42525 standard; DNA; 4046 BP.		
XX	AC	AAQ42525;	
XX	AC		
DT	25-MAR-2003 (updated)		
DT	14-SEP-1993 (first entry)		
XX	Cardiac adenylyl cyclase gene.		
DE			
XX	Regulation; cardiac function; heart; heart failure; ss.		
KW			
XX	Canis familiaris.		
OS			
XX			
Key	Location/Qualifiers		
FH	131..3627		
CDS	/*tag= a		
FT			
XX			
XX	EP543137-A1.		
XX			
PD	26-MAY-1993.		
XX			
PF	12-OCT-1992; 92EP-011737A.		

XX 18-NOV-1991; 91US-0793961.
 XX (AMCY) AMERICAN CYANAMID CO.
 XX Ishikawa Y;
 XX WPI; 1993-168873/21.
 DR P-P8DB; AAR37309.
 XX Purified DNA encoding cardiac adenylyl cyclase - useful to screen
 PT for cpds. which stimulate activity of the cyclase
 XX Claim 1; Fig 2; 34pp; English.
 XX A canine heart cDNA library was constructed in lambda gt10 and was
 CC screened with a 970 bp *BatI*-*HincII* fragment from type I adenylyl
 CC cyclase cDNA probe (encodes the first cytoplasmic domain of adenylyl
 CC cyclase, which has significant homology to other previously known
 CC types of adenylyl cyclase). One positive clone, of 5.4 kb was obtd.
 CC Positive colonies were subcloned into pUC18 and further subcloned
 CC and sequenced bidirectionally. The 5.4 kb clone was used to
 CC rescreen the library and on overlapping clone contg. the 5' end of
 CC the gene was isolated. Together the two clones cover the complete
 CC canine cardiac adenylyl cyclase gene. The gene is suspected of
 CC being involved in the regulation of cardiac function and it is thought
 CC that decreased activity of adenylyl cyclase in the heart may be a
 CC major factor in the development of heart failure. Thus the adenylyl
 CC cyclase gene is useful to screen cpds. which stimulate the activity
 CC of the cyclase.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 4046 BP; 743 A; 1206 C; 1254 G; 843 T; 0 other;
 SQ

Query Match 86.1%; Score 3057.6; DB 14; Length 4046;
 Best Local Similarity 91.9%; Pred. No. 0;
 Matches 3264; Conservative 0; Mismatches 279; Indels 9; Gaps 3;

QY 1 ATGTGATGTTAGTGGCTCTGCTGCTTAAAGTGGATGAACGGAACACGCTGGGT 60
 DB |||||
 QY 61 GAACGCAATGGCAGAGCGTTCCGGCGCCGCTGGCACTCGGGCAGGTGGCTTCTGCAG 120
 DB |||||
 QY 191 GAACGCAATGGCAGAGCGT---CCACGCCCGGGACTCGGACGAGTGGCTTCTGCAG 247
 DB |||||
 QY 121 CCCCCTATATAGTGGCTCTCGGATGACAGACCCACGACCCCTCGCGGCCCC 180
 DB |||||
 QY 248 CCCCCTATATAGTGGCTCTCGGATGACAGACCCCGGAGTCCACCCCTCGCGCTCC 307
 DB |||||
 QY 181 CCTCGTGGCTTGGCAGATGACGCTTTCATCCGGAGGGCGGCCAGGCAAGGGCAAG 240
 DB |||||
 QY 308 CCTCGTGGCTTGGCAGATGAGGCTTTCATCCGGAGGGCGGCCCGGCAAGGGCAAG 367
 DB |||||
 QY 241 GAGCTGGGGCTCGGGCAGTGGCCCTTGGGCTTTCGAGGATPACCGAGGTGAACAACGAC 300
 DB |||||
 QY 368 GAGCTGGGGCTCGGGCAGTGGCCCTTGGGCTTTCGAGGACACTGAGG---CCATGT 424
 DB |||||
 QY 301 GCGGGACGGCTGAGTGGCGCCCGACGCGGTGCCAGAGTGGGGATCTGTGTCGCGC 360
 DB |||||
 QY 425 GTTGGGGACGCTGGAGGTGGCCCTGACGCTGACCCCGGAGTGGGCGATCTGTGTCGCGC 484
 DB |||||
 QY 361 CGTCTGGTGCAGGTGTTCCAGTGAAGCAGTTCCTGGCTTGGCCCAAGCTGGAGCGCTGTAC 420
 DB |||||
 QY 485 CGTCTGGGCCAGGTGTTCCAGTGAAGCAGTTCCTGGCTTGGCCCAAGCTGGAGCGCTGTAC 544
 DB |||||
 QY 421 CAGCGGTACTTCTTCAGATGAACACAGACAGCAGCTGACGCTGCTGATGGCGGTGCTGGTG 480
 DB |||||
 QY 545 CAGCGGTACTTCTTCAGATGAACACAGACAGCAGCTGACGCTGCTGATGGCGGTGCTGGTG 604
 DB |||||
 QY 481 CTGCTCAGCGGTGCTGGCTTTCAGCGCGACCCCGCCCTCAGCTCGCTAT 540
 DB |||||
 QY 605 CTGCTGACAGCGGTGCTGTAGCTTTCATGTGACACCTGCGCCCGCTCAGCTCGCTAC 664
 DB |||||

QY 541 GTGGCACTGTTGGCTGTGCGCCCTCTGTCGGGCTCATGTGGTGTGTAAACCG 600
 DB |||||
 QY 601 CATAGCTTCCGCCAGGACTCCATGTGGGTGAGTTAGTGGTGTCTGGGCATCTCTGGCG 660
 DB |||||
 QY 725 CACAGCTTTCGCCAGGACTCCATGTGGGTGAGTACGTGGTGTCTGGGCATCTCTGGCA 784
 DB |||||
 QY 661 GCGATGCAAGTCCGGGGGCTCTCCAGCAGACCCGCGAGCCCTCTGCGGGCTCTGG 720
 DB |||||
 QY 785 GCGGTTCAGGTGGGGGTGCCCTGGCAGCAACCCCGCAGCCCTCTGTGGGCTCTGG 844
 DB |||||
 QY 721 TGCCCTGTGTTCTTTGTCTACATCCCTACAGCTCTCTCCCATCCGATCGGGGTGCG 780
 DB |||||
 QY 845 TGCCCTGTGTTTGTCTACATCACTTACAGCTCTCTACCATCCGATCGGGCAGCT 904
 DB |||||
 QY 781 GTCTCAGCGGCTGGGCTCTTCCACCTTGATGATTTGATTTGGCTGGCACTTAAACCT 840
 DB |||||
 QY 905 GTCTTCAGTGGCTGGGCTGTCCACCTGATTTGATTTGGCTGGCACTCAACCGC 964
 DB |||||
 QY 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCAATGTGCTGCTCTCTGCAACAC 900
 DB |||||
 QY 965 GGTGAGCTTCTCTGGAAGCAGCTCGGTGCAACATGCTGCTCTCTGCAACAC 1024
 DB |||||
 QY 901 GTCTTGGCATCTGCACACACTATTCAGCAGAGGTGTCTCAGCGCAGGCTTTCAGGAG 960
 DB |||||
 QY 1025 GTCTTGGCATCTGCACACACTTACCCAGCTGAGGTCTCTCAGCGCAGGCTTTCAGGAG 1084
 DB |||||
 QY 961 ACCCGCGTTTACATCCAGGCGCGCTCCACTGACGATGAGAAATCGGACAGGAGCGG 1020
 DB |||||
 QY 1085 ACCCGCGTTTACATTCAGGCGCGCTGCACCTGCCAGATGAGAACCGGAGGAGCGG 1144
 DB |||||
 QY 1021 CTGCTGCTGTGGTATTGCCCCCAGCAGCTTGGCATGGAGATGAAGAAGACATCAACACA 1080
 DB |||||
 QY 1145 CTGCTGCTGTGGTGTGCCCCCAGCATGTTGCCATGAGATGAAGAAGATATCAACACA 1204
 DB |||||
 QY 1081 AAAAAAGAGACATGATGTTCCAAAGATCTACATACAGAGCATGACAAATGTGACGATC 1140
 DB |||||
 QY 1205 AAAAAAGAGACATGATGTTCCAAAGATCTACATCCAGAGCATGACAAATGTGACGATC 1264
 DB |||||
 QY 1141 CTGTTTGAGACATTTAGGGCTTCCAGGCTGGCATCCAGCTGACATCCGACGAGGCTG 1200
 DB |||||
 QY 1265 CTGTTTGAGACATTTGAAGGCTTCCAGGCTGGCTGCCAGTCCAGCGCAGGAGCTG 1324
 DB |||||
 QY 1201 GTCATGACCTTGAATGAGCTCTTTCGCCCGGTTTGAAGAGCTGGCTGCGGAGATCACTGC 1260
 DB |||||
 QY 1325 GTCATGACCTTGAAGAGCTCTTTCGCCCGGTTTGAAGAGCTGGCTGCGGAAATCACTGC 1384
 DB |||||
 QY 1261 CTGAGGATCAAGATCTTGGGGGACTGTTTACTGTGTGTGAGGCTGCGGAGGCGCGG 1320
 DB |||||
 QY 1385 CTGAGGATCAAGATCTTGAAGGACTGTTTACTGTGTGTGAGGCTGCGGAGGCGCGG 1444
 DB |||||
 QY 1321 GCGGACCATGCCCACTGCTGTGTGGAGATGGGGGTGAGCATGATTTAGGCGCATCTCTCGCTG 1380
 DB |||||
 QY 1445 GCAGACCATGCCCACTGCTGTGTGGAGATGGGGGTGAGCATGATCGAGGCCATCTCTCGCTG 1504
 DB |||||
 QY 1381 GTACGTGAGTGAACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCTG 1440
 DB |||||
 QY 1505 GTGCGTGAAGTGAACAGGTGTGAACATGCGCGTGGGCATCCACAGCGGGCGCTG 1564
 DB |||||
 QY 1441 CACTGCGCGCTCTTGGCTTGGGAAATGGCAGTTCGATGTGTGTGTGCTCAATGATGTGACC 1500
 DB |||||
 QY 1565 CACTGTGTGTCTTGGCTGCGGAAATGGCAGTTCGACGTGTGTGTGTCAATGACGTGACT 1624
 DB |||||
 QY 1501 CTGGCCAAACCATGAGGAGGCGCGGCTGSCCGCATCCACATCACTCGGGCAACA 1560
 DB |||||
 QY 1625 CTGGCCAAACCATGAGGAGGCGCGGCTGSCCGCATCCACATCACTCGGGCCAGC 1681
 DB |||||
 QY 1561 CTGCACTGATGAGCGGGGACTTACAGGTGAGCGGCGCTGTGTGGGAGCGGCAACCGG 1620
 DB |||||
 QY 1682 CTGCACTGATGAGCGGGGACTTACAGGTGAGCGGCGCGCTGTGTGGGAGCGGCAACCGG 1741
 DB |||||

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QY 1621 TACCTCAAGGAGCAGCAATTGAGACTTCTCATCTCTGGCGCGCAGCCAGAAACGGAAA 1680
DB 1742 TACCTCAAGGAGCAGCACATCGAGACTTCTCATCTCTGGAGCGCAGCCAGAAACGGAAA 1801
QY 1681 GAGAGAAAGGCATGCTGGCCAGCTGCGAGGAGCTCGGGCCAACTCCATGGAAGGGCTG 1740
DB 1802 GAGAGAAAGGCATGCTGGCCAGCTGCGAGGAGCTCGGGCCAACTCCATGGAAGGGCTG 1861
QY 1741 ATCCGCGCTGGGTTCTGATCGTGGCTTCTCCCGGACCAAGGACTCCAAAGGCTTCCGC 1800
DB 1862 ATCCGCGCTGGGTTCTGATCGTGGCTTCTCCCGGACCAAGGACTCCAAAGGCTTCCGC 1921
QY 1801 CAGATGGGCATGATGATTCAGCAAGACAAACCGGGGACCCCAAGATGCCCTGAAACCT 1860
DB 1922 CAGATGGGCATGATGATTCAGCAAGACAAACCGGGGATGCCCAAGATGCCCTGAAACCT 1981
QY 1861 GAGATGAGGTGATGATGATTCAGCGGTGCGCATCGATCGCGCAGCATGATCAGCTG 1920
DB 1982 GAGATGAGGTGATGATGATTCAGCGGTGCGCATCGATCGCGCAGCATGATCAGCTG 2041
QY 1921 GAGAGGACCATGTCGCGGTTCTGCTCACCTTCCAGAGAGAGATCTTGAGAGAG 1980
DB 2042 CGAAGAGACCATGTCGCGGTTCTGCTCACCTTCCAGAGAGAGATCTTGAGAGAG 2101
QY 1981 TACTCCCGGAAGGTGGATCCCGCTTCGAGACCTTACGTTGCTGTGCTGCTGTTGGTCTTC 2040
DB 2102 TACTCAAGGAAGGTGGATCCCGCTTCGAGACCTTACGTTGCTGTGCTGTTGGTCTTC 2161
QY 2041 TGCTTCATCTGTTTCACTCAGCTTCTCATCTTCCACACATCCACCTGATGCTTGGGATC 2100
DB 2162 TGCTTCATCTGTTTCACTCAGCTTCTCATCTTCCACACATCCACCTGATGCTTGGGATC 2221
QY 2101 TATGCCAGCATCTTCTGCTGCTGCTAATCACCGTGTGATCTGTGCTGTGCTGCTCTGT 2160
DB 2222 TACGCCAGTATCTTGTGCTGCTGCTAATCACCGTGTGATCTGTGCTGTGCTGCTCTGT 2281
QY 2161 GGTTCCTGTTCCCTAAGGCCCTGCAACGCTGTGCTCCGAGCATTTGCTCCGCTCACGGCA 2220
DB 2282 GGTTCCTGTTCCCTAAGGCCCTGCGAGCTTTTCCCGCAGCATCGTCCGCTCTCGGGCA 2341
QY 2221 CATAGCACCGAGTGTGGATCTTTTCCGCTGCTGCTGCTGTTTACTTCTGCGCATTGCCAAC 2280
DB 2342 CACAGCATGCTGGTGTGGATTTTTCAGTCTGCTGATGTTTCACTCTGCGCATCGCCAAC 2401
QY 2281 ATGTTACCTGTAAACACACCCCATACGAGCTGTGCGCCGAGTGTGCTGCTGCTGCTGCT 2340
DB 2402 ATGTTACCTGTAAACACACCCCATACGAGCTGTGCGCCGAGTGTGCTGCTGCTGCTGCT 2461
QY 2341 CCTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
DB 2462 CCGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2521
QY 2401 CCGCTGCTGAGGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
DB 2522 CCGCTGCTGAGGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2581
QY 2461 CTGCTGATCTCTTGGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
DB 2582 CTGCTGATCTCTTGGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2641
QY 2521 ATGATCTTTGCTTGGGGCTCATCTATTGCTGCTGCTTCTGCTGGGTCCTCCAGCCACC 2580
DB 2642 ATGATCTTTGCTTGGGGCTCATCTATTGCTGCTGCTTCTGCTGGGTCCTCCAGCCACC 2701
QY 2581 ATCTTTGACAACTATGACCTTATGCTTGGGCTCATGCTTGGCTTCTTCCAAATGAGACC 2640
DB 2702 ATCTTTGACAACTATGACCTTATGCTTGGGCTCATGCTTGGCTTCTTCCAAATGAGACC 2761
QY 2641 TTTGATGGGCTGAGCTGCTCAGCTGCGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
DB 2762 TTTGATGGGCTGAGCTGCTCAGCTGCGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2821
QY 2701 ATTCTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
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DB 2822 ATTCTGCTGCTGTTTGGCCCTGGCGCTGTATCTGACGCCAGCAGGTGGAAATCAACTGCA 2881
QY 2761 CGCTAGACTTCTCTCTGGAATACTACAGGCAACAGGGGAGAGGAGAGATGGAGGAGCTA 2820
DB 2882 CGTCTGAGACTTCTCTGGAATACTGCAAGGCAACGGGGGAGAGGAGAGATGGAGGAGCTC 2941
QY 2821 CAGGCATACAAACCGGAGGCTGCTGCAATAACATTTCTGCCCAAGGACGCTGGCGGCCACTTC 2880
DB 2942 CAGGCCTACAAACCGAGAGCTGCTGCAATAACATTTCTGCCCTAAGGACGCTGGCTGCCACTTC 3001
QY 2881 CTGGCCCGGAGCGCCGCAATGATGAATCTCTATCATGCTGCTGCTGCTGCTGCTGCTGCT 2940
DB 3002 CTGGCCCGGAGCGCCGCAACGATGAGCTCTACTACAGTCTGCTGCTGCTGCTGCTGCTGCT 3061
QY 2941 ATGTTTTCCTCCATTCGCCAATCTCTGAGTTCTATGCTGAGCTGGAGGCAAAACAAATGAG 3000
DB 3062 ATGTTTTCCTCCATTCGCCAATCTCTGAGTTCTATGCTGAGCTGGAGGCAAAACAAATGAG 3121
QY 3001 GGTGTCGAGTCTGCGGCTGCTCAACAGATCATCGCTGACTTTTGTATGATGATTTATCAGC 3060
DB 3122 GGTGTCGAGTCTGCGGCTGCTCAACAGATCATCGCTGACTTTTGTATGATGATTTATCAGC 3181
QY 3061 GAGGACGCTTCCGCGAGCTGGAAAGATCAAGACGATTTGCTAGCACCTTACATGCTGCTGCT 3120
DB 3182 GAGGACGCTTCCGCGAGCTGGAAAGATCAAGACGATTTGCTAGCACCTTACATGCTGCTGCT 3241
QY 3121 TCAGGCTGAAACGCCAGCCTTACGATCAGTGGCGGCTCCACATCATCTGCTGCTGCTGCT 3180
DB 3242 TCAGGCTGAAACGCCAGCCTTACGATCAGTGGCGGCTCCACATCATCTGCTGCTGCTGCT 3301
QY 3181 GACTAGCCATGCGGCTCATGAGCAGATGAAGCAGATCAATGAGCAGCTCTTCAACAAT 3240
DB 3302 GACTAGCCATGCGGCTCATGAGCAGATGAAGCAGATCAATGAGCAGCTCTTCAACAAT 3361
QY 3241 TTCAGATGAAGATTTGGCTGAAACATGGGCCAGTCTGTCGAGCTGTCATGCGGCTCGG 3300
DB 3362 TTCAGATGAAGATTTGGCTGAAACATGGGCCAGTCTGTCGAGCTGTCATGCGGCTCGG 3421
QY 3301 AAGCCACATGATGACATCTGGGGGACACAGTGAATGCTCTAGTCTGATGAGCAGCAGC 3360
DB 3422 AAGCCACATGATGACATCTGGGGGACACAGTGAATGCTCTAGTCTGATGAGCAGCAGC 3481
QY 3361 GGGGTCTCCGACCGAATCCAGGTGACACGAGCTCTGACGAGTCTTAGCTGCGCAAGGGC 3420
DB 3482 GGGGTCTCTGACCGAATCCAGGTGACACGAGCTCTGACGAGTCTTAGCTGCGCAAGGGC 3541
QY 3421 TACAGCTGAGTGTGAGGGTGGTCAAGGTGAAGGGCAAGGGGAGAGATGACCACTAC 3480
DB 3542 TACAGCTGAGTGTGAGGGTGGTCAAGGTGAAGGGCAAGGGGAGAGATGACCACTAC 3601
QY 3481 TTCCTCAATGGGGGCGCCAGCAGTTAACAGGGCCAGCCCAATTTACAGCTGAAGGGACC 3540
DB 3602 TTCCTCAATGGGGGCGCCCGCCAGTTAGCAGACCGCTACAAAGTTTCAAGCTGTCAGGACC 3661
QY 3541 AAGGTGGGCACT 3552
DB 3662 AAGGTGGGCACT 3673
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RESULT 9

ABI99680

ID ABI99680 standard; cDNA; 5841 BP.

XX ABI99680;

XX 07-MAR-2002 (first entry)

XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:716.

XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

XX vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.

XX

OS Mus musculus.
 XX WO200188188-A2.
 XX 22-NOV-2001.
 XX 18-MAY-2001; 2001WO-JP04192.
 XX 18-MAY-2000; 2000JP-0145977.
 XX (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX WPI; 2002-034733/04.
 XX P-PSDB; ABB57257.
 XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or
 PT by determining the expression profile of a gene group comprising these
 PT genes -
 XX Claim 2; Page 1771-1780; 2690pp; English.
 XX The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding
 CC the protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The
 CC expression levels or expression profiles produced by these genes are
 CC used as an indicator when screening for ischaemic condition-improving
 CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
 CC represent PCR primers for a mouse ischaemic condition related sequence,
 CC which are used in the exemplification of the present invention.
 XX Sequence 5841 BP; 1214 A; 1558 C; 1673 G; 1396 T; 0 other;
 SQ

Query Match 79.3%; Score 2816.2; DB 24; Length 5841;
 Best Local Similarity 87.8%; Pred. No. 0;
 Matches 3120; Conservative 0; Mismatches 423; Indels 10; Gaps 4;

QY 1 ATGTCATGTTAGTGGCTCTCTGCTCCCTAAAGTGGATGACGGAACACAGCTTGGGGT 60
 DB |||||
 QY 61 GAACGCAATGGCAGAGCGTTTCGGCGCGCGCTGGCAGCTCGGGCAGGTGGCTTCTGCACG 120
 DB |||||
 QY 156 GAACGCNATGGCAGAGCG---CCACGCCACGGGATCGAGCCAGTGGCTTCTGCACA 212
 QY 121 CCCCGCTATATAGTGGCTCTCGGATGACAGACCAACAGCCACCCCTGCGGGCCCC 180
 DB |||||
 QY 213 CCTCGCTACATGAGCTGCTCAAGATGCGAGCCACCCAGCCCCACCTCTGACGCTCAC 272
 QY 181 CCTCGGTGCCCTGACAGATGACGCTTATCGGAGGGGGCGGCCAGGAGGGCAAG 240
 DB |||||
 QY 273 ACTCGGTGCCCTGACAGATGAAGCTTTCATCAGAGAGGGGGCGGCCCGGAGGGGGTGTG 332
 QY 241 GAGCTGGGGCTGCGGCGAGTGGCTTCTGGCTTCGAGGATACCGAGGTGACACGACAGCG 300
 DB |||||
 QY 333 GAGCTGGGGCTGCGGTGAGTGGCTTGGGTTTGACGACATGAGGTGACACACCGATG 392
 QY 301 GCGGGAAGCTGAGGTGGCGCCGACGCGGTGCCAGAGTGGCGCATCTCTGCTGGCGC 360
 DB |||||
 QY 393 GGC---ACAGCTGAAGTGGCACCAGATACATCGCTCGAGCGGTCCGTCTCTGCTGGCAC 449
 QY 361 CGTCTGGTGCAGGTGTTCCAGTGCAGACAGTTCGTTCCGGCCAAAGCTGGAGGCGCTGTAC 420
 DB |||||
 QY 450 CGGCTTGTGCAGGTGTTCCAGTCTAAGCAGTTCCTGCTCTGCGCAAGCTGGAGCGGCTGTAC 509

QY 421 CAGCGTACTTCTCCAGATGAACAGAGCAGCCTGACGCTGCTGATGGCGGTGCTGCTG 480
 DB |||||
 QY 510 CAGCGTACTTCTCCAGATGAACAGAGCAGCCTCAGCCTGCTCATGCGGGTGTGCTG 569
 DB |||||
 QY 481 CTGCTCAGCAGCGGTGCTGCTGGCTTTTCCACGCGGACCCCGCGCCCTCAGCCTGCTGAT 540
 DB |||||
 QY 570 CTGCTCATGGCTGTACTGTTGACTTTCACGCTGCGCTGCGCCAGCCTCAGCCTGCTTAC 629
 DB |||||
 QY 541 GTGGCAGTGTGGCTGCGCGCCCTGTTTCGTGGGGCTCATGCTGGTGTGTAACCGG 600
 DB |||||
 QY 630 GTGGCCCTGCTGACCTGTGCTCTGTCTTTTGTGGTACTCATGGTGTGTAACCGA 689
 DB |||||
 QY 601 CATAGCTTCCGCCAGGACTCCATGTGGTGTGAGTTACGTGGTGTGCTGGGCATCTCGCG 660
 DB |||||
 QY 690 CACAGCTTCCGCCAGGACTCCATGTGGGTGTGAGCTATGTGCTCTGGGCATCTTAGCA 749
 DB |||||
 QY 661 GCAGTGCAGTGTGGGGGGCTCTCGCAGCAGACCCCGCGCAGCCCTCTGCGGGCTCTGG 720
 DB |||||
 QY 750 GCGGTGCAAGTGGGGGTGCGCTGCGCAGCAATCCACACAGCCCTCGCGGGCGCTTGG 809
 DB |||||
 QY 721 TGCCCTGTGTTTGTCTACATCGCTTACACGCTTCTCCCATCCGATCGGGCTGCC 780
 DB |||||
 QY 810 TGCCCGGTGTTCTGCTATACCTACCTACTCTTCTCCCATTCGATCGGAGCCGA 869
 DB |||||
 QY 781 GTCTCTCAGCGGCTGGGCTCTCTCCACCTTGATCTTGGCTGGCACTTAACCGT 840
 DB |||||
 QY 870 GTACTCAGCGGCTGGGCTCTCTACTCTGATCTGATTTGGCTGGCAGCTCAACAGC 929
 DB |||||
 QY 841 GGTGATGCTTCTCTGGAAGCAGCTCGTGGTCCCAATGTGTGCTGTTCTCTGCAACCAAC 900
 DB |||||
 QY 930 AGCAGCCCTTCTTGTGAAGCAGCTCGTGTCTAACGTGTGCTCTCTCTGCAACCAAT 989
 DB |||||
 QY 901 GTCTATGGCATCTGCACACATCTCCAGCAGAGTGTCTCAGCGCCAGGCTTTCAGAG 960
 DB |||||
 QY 990 GCCATCGGTGTGACACACATACCTCTGAAAGTGTCTCAGCGCCAAAGCTTTCAGGAG 1049
 DB |||||
 QY 961 ACCCGCGTTATACATCCAGGCGCGCTCCACCTGAGCATGAGATTCGCGCAGCAGGCGG 1020
 DB |||||
 QY 1050 ACCCGAGTTATACATCCAGGCGCGCTGCACCTGAGCATGAGACCGTTCAGCAGGAACG 1109
 DB |||||
 QY 1021 CTGCTGTGTCGGTATTTGCCCGCAGCAGTTCGCCATGGAGATGAAGAAGACATCAACACA 1080
 DB |||||
 QY 1110 CTGCTGTATCGTGTGTGCCCCCAGCAGCTTGCCTATGAGATGAAGAAGACATCAACACA 1169
 DB |||||
 QY 1081 AAAAAAGAGACATGATGTTCCACAGATCTACATACAGAGCATGCAATGTGAGCATC 1140
 DB |||||
 QY 1170 AAAAAAGAGACATGATGTTCCATAGATCTACATCCAGAGCATGATTAATGTGAGCATC 1229
 DB |||||
 QY 1141 CTGTTTGCAGACATTTAGGGGCTTCCACAGCTGGCATCCAGTGCACCTGCGCAGGAGCTG 1200
 DB |||||
 QY 1230 CTGTTTGGGACATTTAGGGGCTTCCACAGCTTGGCTTCCAGTGCATGCAAGGACATG 1289
 DB |||||
 QY 1201 GTCATGACCTTGAATGAGCTCTTTGCCGGTTTGAAGCTGGTGTGCGGAGAAATCACTGC 1260
 DB |||||
 QY 1290 GTCATGACCTTGAATGAGCTCTTTGCCGGTTTGAAGCTGGTGTGCGGAGAAATCACTGT 1349
 DB |||||
 QY 1261 CTGAGGATCAGATCTTTGGGGAGCTTACTACTGTGTGTCAGGGCTTCCCGAGGCGCCGG 1320
 DB |||||
 QY 1350 CTGAGGATCAAGATCTTTAGGAGCTGTACTACTGCGTGTGAGGGCTTCCCGAGGCGCCGG 1409
 DB |||||
 QY 1321 GCCACCATGCGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1380
 DB |||||
 QY 1410 GCAGATCAGCGCCACTGCTGTGTGGAGATGGGGGTAGACATGATCGAAGCCATCTCGCTG 1469
 DB |||||
 QY 1381 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCTG 1440
 DB |||||
 QY 1470 GTGCGTGAAGTAAACAGGTGTGAACATGCGTGTGGGCATCCACAGCGGACGTGTG 1529
 DB |||||
 QY 1441 CACTGCGGCTGCTTGGCTTGGGAATGGCAGTTCGATGTGTTGTTGTTCAATGATGTGACC 1500
 DB |||||
 QY 1530 CATTCGCGGCTGCTTGGCCTACGGAATGGCAGTGTGATGTCTGTTCAACAGTGTGACC 1589
 DB |||||
 QY 1501 CTGCGCAACCATGAGGAGGAGGCGCGGCTGCGCATCCACATCACTCGGCGCAACA 1560

[illegible]

Db	2667	ATCTTTGACAACTATGATCTACTGTTGGCGTCCATGGCTTCTCCTCCATGAGACC	2722
Qy	2641	TTTGATGGGCTGGAGCTGCTCCAGCTGCGAGGAGGGTGCCCTCAAATATATGACCCCTGTG	2700
Db	2727	TTTGATGGGCTGGAGCTGCCCAGCTGTGGGAGGGTAGCGCTCAAATATATGACCCCGTG	2786
Qy	2701	ATTCTGCTGTGTTTGGCTTGGCGCTGTATCTGATGCTCAGCAGGTGGAGTGCATCTGCC	2760
Db	2787	ATTCTGCTGTGTTTGGCCCTGGCACTGTATCTGCATGTCACACAGGTGGAAATGCAGCTGCC	2846
Qy	2761	CGCTAGACTTCCTCTGGAAACTACAGGCAACAGGGGAGAGGAGAGATGGAGGAGCTA	2820
Db	2847	CGCTAGACTTCCTCTGGAAAGTTACAGGCAACAGGGGAGAGGAGAGATGGAGGAGCTA	2906
Qy	2821	CAGGCATACAACCGGAGGCTGCTGCATAACATTTCTGCCCAAGGACGTGGCGGCCCACTTC	2880
Db	2907	CAGGCATACAACCGGAGGTTGCTGCATAACATTTCTTCCCAAGGACGTGGCGGCCCACTTC	2966
Qy	2881	CTGGCCCGGAGCGCCGCAATGATGAATCTACTATCAGTCTGTGTGAGTGTGTGGCTGTT	2940
Db	2967	CTGGCCCGGGAACGCCGCAACGATGAGCTGTACTACCACTGCTGTGAAATGTGTGGCTGTC	3026
Qy	2941	ATGTTTTCCTCCATTTGCTCAACTTCTCTGAGTTCTTATGTGAGCTGGAGGCAAAACAATGAG	3000
Db	3027	ATGTTTTCCTCCATTCGCCAAATTTCTCGAGTTCTTACGTGAGCTCGAGGCAAAACAAGAG	3086
Qy	3001	GGTGTGCAGTGCCTTGGCGCTGCTCAACGAGATCATCGCTGACTTTGATGAGATTAATCAGC	3060
Db	3087	GGCGTGGAGTGCCCTGGCGCTGCTCAATGAGATCATCGCAGACTTTGACGAGATCATCAGT	3146
Qy	3061	GAGGAGCGGTTTCGGGACGTGGAAAAGATCAAGACGATTTGGTAGCACTACATGGCTGCC	3120
Db	3147	GAGGAGAGATTTCGGGCAAGTTTGGAGAAGATCAAGAACCATCGGTAGCACTACATGGCGGCC	3206
Qy	3121	TCAGGGCTGAACGCGCAGCACCTACGATCAGTGGCGCGCTCCACATCACTGCGCCTGGCT	3180
Db	3207	TCTGGGCTAAATGCCAGCACCTATGACAGGTGCGCGCGCTCACACATCAGCGCGCTGGCT	3266
Qy	3181	GACTACGCCATCGGCTCATGGAGCAGATGAAGCACATCAATGAGCACTCTTCAACAAT	3240
Db	3267	GACTATGCCATCGGCTCATGGAGCAGATGAAGAACACATCAATGAACACTCTTTCAACAAT	3326
Qy	3241	TTCCAGATGAAGATTGGCTGAACATGGGCCCCAGTCTGTGCAGGTGTCACTCGGGCTCGG	3300
Db	3327	TTCCAGATGAAGATCGGGTTGAACATGGGTCGCGTGTAGCAGCGCTCATTTGGGCGCCGA	3386
Qy	3301	AAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGTCCGTATGGACAGCAGC	3360
Db	3387	AAGCCACAGTATGACATCTGGGGAATACCGTGAAATGTTTCCAGTCTGTATGGACAGCACT	3446
Qy	3361	GGGTCGCCCAACCGAATCCAGGTGACCAACGGAATCTGTACAGGTTCTAGCTGCCAAGGGC	3420
Db	3447	GGAGTTCTTCACCGAATACAGGTGACTACGGAATATACCAAGGTTCTTAGCTGTCGAAGGGC	3506
Qy	3421	TACCAGCTGGAGTCTCGAGGGTGGTCAAGGTGAAGGCAAGGGGAGATGACCACTAC	3480
Db	3507	TACCAGCTGGAGTCTCGAGGGTGGTCAAGGTGAAGGGAAGGGGGAGATGACCACTAC	3566
Qy	3481	TTCTCTCAATGGGGCCCCCAGCAGTTAAACGGGCCCCAGGCCAC-AAAATTTCAGCTGAAGGGAC	3539
Db	3567	TTCTCTCAACGGGGCCCCCAGCAGTTAGCAGATGCACAGCTGAGATTCAACCGAAGGAC	3626
Qy	3540	CAAGGTGGGCACT	3552
Db	3627	CAAGGTGGGCACT	3639

RESULT 10
AAA53923
ID AAA53923 standard; CDNA; 4131 BP.
XX
AC AAA53923;
XX

1321 GCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTTGAGGCCATCTCGCTG 1380
1370 GCAGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATCGAGGCCATCTCGCTG 1429
1381 GTAGCTGAGGTGACAGGTGTGAATGTGAACATGCGGTGGGCAATCCACAGCGGGCGGTG 1440
1430 GTGCGTGAAGTAAACGGGTGTAATGTGAACATGCGGTGGGCAATCCACAGCGGGCGGTGTA 1489
1441 CACTGCGGCTGCTTGGCTTGGCGAATGCGAGTTGATGTGTGGTCCCAATGATGTGACC 1500
1490 CACTGCGGCTGCTTGGCTTGGCGAATGCGAGTTGATGTGTGGTCCCAATGATGTGACC 1549
1501 CTGGCCAAACACATGAGGAGGAGCGCGGCTGGCGCATCCACATCACTCGGGCAACA 1560
1550 CTGGCCAAACACATGAGGAGGAGCGCGGCTGGCGCATCCACATCACTCGGGCCACA 1609
1561 CTGCACTGACCTGAACCGGGACTACAGGTGAGCCAGCGCGTGTGGCGAGCGCAACGCG 1620
1610 CTGCACTGACCTGAACCGGGACTACAGGTGAGCCAGCGCGTGTGGCGAGCGCAACGCG 1669
1621 TACTCTAAGGAGCAGCATGAGACTTCTCATCTGGCGGCCAGCGAGCAACGGAAA 1680
1670 TACCTCAAGGAGCAGCATGAGACTTCTCATCTGGCGGCCAGCGAGCAACGGAAA 1729
1681 GAGGAGAAAGCCATGCTGGCCAAAGCTCAGCGGACTCGGGCCAACTCCATGGAAGGCTG 1740
1730 GAGGAGAAAGCCATGCTGGTCAAGCTCAGCGGAGCGCGGCCAACTCCATGGAAGNCTG 1789
1741 ATGCGCGCTGGGTCTGATGCTGCTTCTCGCGAACAGGACTCAAGGCTTCCGC 1800
1790 ATGCGCGCTGGGTCTGATGCTGCTTCTCGCGAACAGGACTCAAGGCTTCCGA 1849
1801 CAGATGGGCTGATGATTCAGCAAGAGCAACCGGGGCAACCAAGTCCCTGAAACCT 1860
1850 CAGATGGGCTGATGATTCAGCAAGAGCAACCGGGGTCGCGGAGTCTGTAACCT 1909
1861 GAGGATGAGGTGATGATTCAGCAAGAGCAACCGGGGCAACCAAGTCCCTGAACTG 1920
1910 GAGGATGAGGTGATGATTCAGCAAGAGCAACCGGGGCAACCAAGTCCCTGAACTG 1969
1921 CGGAAGACCATGTCGCGGCTTCTGCTCACTTCAGAGAGAGATCTTGAGAGAAG 1980
1970 CGTAAGGACCATGTCGCGGCTTCTGCTCACTTCAGAGAGAGATCTTGAGAGAAG 2029
1981 TACTCCGGAAGTGGATCCCGCTTCGGAGCTTACGTTGCTGCTGCTGCTGCTGCTTC 2040
2030 TATTCAGGAAAGTAGACCTCGTTCGAGGCTTACGTTGCTGCTGCTGCTGCTGCTTC 2089
2041 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCACACTCCACCTGATGCTTGGGATC 2100
2090 TGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCACACTCCCGCTGATCTCGGAT 2149
2101 TATGCCAGCATCTTCTGCTGCTAAATCAACGCTGCTGATCTGCTGCTGCTGCTGCT 2160
2150 TATGCCGGAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2209
2161 GGTTCCTGCTTCCCTAAGGCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
2210 GGGTCTTCTTCCCAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2269
2221 CATAGCACCGCAGTTGGCATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
2270 CACAGCACCGCTGTTGGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2329
2281 ATGTTCACTGTAAACCAACACCCCATACGAGCTGCTGAGCGGATGCTGTAATTTAAACA 2340
2330 ATGTTCACTGTGACACACCCCATACGAGGCTGCTGAGCGGCTGCTGCTGCTGCTGCT 2389
2341 CTTGCTGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
2390 CCGTCCGATGTCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2449

2401 CCCCTGTGTGAGGGCAACCATGCCCCACTCGAGCTTTCTTAGTACTTTCAATCGGGAACATG 2460
2450 CCCCTGTGTGAGGGCAACCATGCCCCACTCGAGCTTTCTTAGTACTTTCTGCGGAGTGTG 2509
2461 CTGCTGAGTCTCTTGGCCAGCTCTGCTTCTTCTGCAATCAGCAGCATCGGGAAGTTGGCC 2520
2510 CTGCTGAGTCTCTTGGCCAGCTCGGCTTCTTCTCACAATCAGCAGCATTTGGCAAGTAGTT 2569
2521 ATGATCTTTGTCTTGGGGCTCATCTATTGTTGGTCTCTTCTGCTGGGTCCCCCAGCCACC 2580
2570 ATGACCTTTGTCTTGGGGTCACTACTACTTGTCTTCTGCTTGTGCGGTCCCCCAGCCACC 2629
2581 ATCTTTGACAACATATGACCTACTGCTTGGCTGCATGCTGCTGCTTCTTCTCAATGAGACC 2640
2630 ATCTTTGACAACATATGATCTACTGCTTACGCTCATGGCTTGGCTTCTTCTCAATGAGACC 2689
2641 TTTGATGGGCTGAGCTGTCCAGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2700
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2761 CGCTTAGACTTCTCTTGGAACTTACAGGCAACAGGGGAGAGGAGGAGGAGGAGGAGGAGG 2820
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2941 ATGTTTGCCTCCATTTGCCAACTTCTCTGAGTTCTATGTGAGCTGAGGAGGAGGAGGAGG 3000
2990 ATGTTTGCCTCCATCGCCAACTTCTCTGAGTTCTATGTGGAACCTGGAGGAGGAGGAGG 3049
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3061 GAGGAGCGGTTCCGGCAGCTGGAAGAGATCAAGAGATTTGTTAGCACTTACATGCTGCTGCT 3120
3110 GAGGAGAGGTTCCGGCAGCTGGAAGAGATCAAGAGATTTGTTAGCACTTACATGCTGCTGCT 3169
3121 TCAGGCTGAAACGCGCAGCACTACGATCAGGTGGGCGCTGCCACATCACTGCTGCTGCTGCT 3180
3170 TCAGGCTGAAATGCGCAGCACTATGACAGGTCGCGCGCTGCGACATCACCGGCTGGCA 3229
3181 GACTAGCCATGCGGCTCATGAGGAGATGAGGAGATCAATGAGGAGTCTTCAACAT 3240
3230 GACTAGCCATGCGGCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3289
3241 TTTCCAGATGAAGATTCGGCTGAACTGCGGCCAGTGTGCGGAGTGTCTGCTGCGGCTGCGG 3300
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3301 AAGCCACAGTATGAGATCTGGGGGAAACAGTGAATGTCTTATGCTGATGAGGAGGAGGAGG 3360
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3410 GGAGTTCTTGAACCGGATACAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3469
3421 TACCACTGAGGTGTGAGGGGTGTTCAAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3480
3470 TACCACTGAGGTGTGAGGGGTGTTCAAGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3529
3481 TTTCTCAATGGGGGCCCCCAGCAGTGAACAGGGGCCA - GCCACAAATTCAGTGAAGGGA 3538

Db

3530 TTCCTCAATGGGGGCCCGACAGTTAGCAGAGCCACGAGTGGAAATTCACCAAAAGGGA 3589

QY 3539 CCAAGGTGGGCACT 3552

Db 3590 CCAAGGTGGGCACT 3603

RESULT 11

AAD08562

ID AAD08562 standard; cDNA; 1812 BP.

AC AAD08562;

04-SEP-2001 (first entry)

Human partial cardiac adenylylcyclase VI (ACVI) isoform #2 cDNA.

Human: cardiac: beta-adrenergic signalling protein: beta-2sp.

KW Human; cardiac; beta-adrenergic signalling protein; beta-ASP;
KW myocardium: gene therapy: beta-adrenergic receptor: beta-AR:

KW myocardin; gene therapy; beta-adrenergic receptor; beta-AR;
KW adenylylcyclase: adenylylate cyclase: cAMP synthetase:

KW adenylyl cyclase; adenylate cyclase; CAMP synthetase;
KW G-protein receptor kinase; GRK: heart disease: congestive hear

cardiac adenylyclase VI: ACVI isoform: beta-ASP transgene: 88

OS Homo sapiens.

XX
 со
 ному вартепв.

FH	Key	Location/Qualifiers
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FN	Key	Location/Quarters
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/ category=

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FT.
/note= "CDS does not

FT /EC_number= "4.6.1.1"

PN WO200148164-A2.

PD 05-JUL-2001.

26-DEC-2000; 2000WO-US35411.

PR 27-DEC-1999: 99US-0472667.

PA (REGC) INTIV CALTEORNTA.

XX
PT
Hammond HK
Gao M.

XX
DB WPT: 2003-418260/44

DR P-PSDB; AAE04309.

PT Novel polynucleotide encoding a modified adenylyl cyclase polypeptide
PT useful for enhancing cardiac function in mammalian hearts, and for
PT treating heart disease, especially congestive heart failure -

PS Example 5; page 115-119; 153pp: English.

The present invention relates to methods and compositions for enhancing cardiac function in mammalian hearts by inserting transgenes encoding beta-adrenergic signalling proteins (beta-ASP) which increase beta-adrenergic responsiveness within the myocardium using *in vivo* gene therapy. The beta-ASPs of the invention include beta-adrenergic receptors (beta-AR), adenylyl cyclases (also referred as adenylylase, adenylylate cyclase and CAMP synthetase) and G-protein receptor kinase (GRK) inhibitors. The beta-ASP is used for enhancing cardiac function in mammalian hearts and for treating heart disease, especially congestive heart failure. The present cDNA sequence encodes human partial cardiac adenylylase VI (ACVI) isoform which is used for generating a third beta-ASP transgene, used in the exemplification of the invention.

Sequence 1812 BP: 361 A: 539 C: 507 G: 405 T: 0 other:

Query Match

Query Match Best Local Similarity Score I/63.4; DB 22; Length 1812; 49.6%; Pred NC 0: 98.7%

BEST LOCAL SIMILARITY 98.7%; Pred. No. 0;
Matches 1789: Conservative 0; Mismatches

636	Qy	TTACGTGGTGTCTGGGCAATCCTGGCGGAGTGCAGTGGGGGGCGCTCTCGACGACAGCC	695
3	Db	TAACGTGGTGTCTGGGCAATCCTGGCGGAGTGCAGTGGGGGGCGCTTTGGCAGACAGCC	62
	Qy	GGCAGCGCCCTCTGGCGGGCTCTGGTGGCCCTGTGTTCTTTGTCTACATCGCTACACGCT	755
63	Db	GGCAGCGCCCTCTGGCGGGCTCTGGTGGCCCTGTGTTCTTTGTATACATCGCATACACGCT	122
756	Qy	CTCTCCCATCCGATCGGGCTGCCCTCTCTCAGCGGCTTGGGCTCTCCACCTTGCATTT	815
123	Db	CTCTCCCATCCGATCGGGCTGCCCTCTCTCAGCGGCTTGGGCTCTCCACCTTGCATTT	182
816	Qy	GATCTTTGGCTGGCAACTTAAACCGTGGTGATGCTCTCTTGAAAGAGCTCGGTGCGAA	875
183	Db	GATCTTTGGCTGGCAACTTAAACCGTGGTGATGCTCTCTTGAAAGAGCTCGGTGCGAA	242
876	Qy	TGTGCTGTCTTCTCTGCACCAACGTCAATTGGCATCTGCACACATATCCAGCAGGT	935
243	Db	TGTGCTGTCTTCTCTGCACCAACGTCAATTAGCATCTGCACACATATCCAGCAGGT	302
936	Qy	GTCTCAGCGCCAGGCCCTTTCAGGAGACCGCGGTATACATCCAGGCGCGCTCCACCTGCA	995
303	Db	GTCTCAGCGCCAGGCCCTTTCAGGAGACCGCGGTATACATCCAGGCGCGCTCCACCTGCA	362
996	Qy	GCATGAAATCGGCAGCAGGAGCGGTGCTGTCTCGTATTTGCCCCAGCAGCTTGCCAT	1055
363	Db	GCATGAAATCGGCAGCAGGAGCGGTGCTGTCTCGTATTTGCCCCAGCAGCTTGCCAT	422
1056	Qy	GGAGATGAAGAAGACATCAACNCAAAAAAAGNAGACATGATGTTCCACNAGATCTACAT	1115
423	Db	GGAGATGAAGAAGACATCAACNCAAAAAAAGNAGACATGATGTTCCACNAGATCTACAT	479
1116	Qy	ACAGAAGCATGACAATGTCAGCATCTGTTTGAGACATTTGAGGGCTTCACCAAGCTTGGC	1175
480	Db	ACAGAAGCATGACAATGTCAGCATCTGTTTGAGACATTTGAGGGCTTCACCAAGCTTGGC	539
1176	Qy	ATCCAGTGCATCGCGCAGGAGTGTGCATGACCCCTGAATGAGCTCTTTGCCGGTTTGA	1235
540	Db	ATCCAGTGCATCGCGCAGGAGTGTGCATGACCCCTGAATGAGCTCTTTGCCGGTTTGA	599
1236	Qy	CAAGCTGGCTCGGGAATCATCTGCTGAGGATCAAGATCTTTGGGGGACTGTTACTCTG	1295
600	Db	CAAGCTGGCTCGGGAATCATCTGCTGAGGATCAAGATCTTTGGGGGACTGTTACTCTG	659
1296	Qy	TGTGTCAGGCTGTCGGAGGCGCGGCGCACCATGCCACTGCTGTGTGAGATGCGGGT	1355
660	Db	TGTGTCAGGCTGTCGGAGGCGCGGCGCACCATGCCACTGCTGTGTGAGATGCGGGT	719
1356	Qy	AGACATGATTGAGCCATCTCGCTGTAGCTGAGGTGACAGGTGTAATGTGAACATGCG	1415
720	Db	AGACATGATTGAGCCATCTCGCTGTAGCTGAGGTGACAGGTGTAATGTGAACATGCG	779
1416	Qy	CGTGGGCATCCACAGCGGCGGTGCACTGCGCGCTCTTGGCTTCGGAAATGGCAGTT	1475
780	Db	CGTGGGCATCCACAGCGGCGGTGCACTGCGCGCTCTTGGCTTCGGAAATGGCAGTT	839
1476	Qy	CGATGTGTGCTCCAAATGATGTGACCTGCGCCACCATGGAGCGAGGCGCGCTCG	1535
840	Db	CGATGTGTGCTCCAAATGATGTGACCTGCGCCACCATGGAGCGAGGCGCGCTCG	899
1536	Qy	CCGCATCCACATCACTCGGGCAACATGCAGTACCTGAAACGGGGACTACAGGTGGAGCC	1595
900	Db	CCGCATCCACATCACTCGGGCAACATGCAGTACCTGAAACGGGGACTACAGGTGGAGCC	959
1596	Qy	AGSCCGTGTGGCGGCAACCGCTGTAATCTCAAGGAGCAGCAATTTGAGACTTTCTCTCAT	1655
960	Db	AGSCCGTGTGGCGGCAACCGCTGTAATCTCAAGGAGCAGCAATTTGAGACTTTCTCTCAT	1019
1656	Qy	CCTGGGCGGCGGCAAGAAACGGAAAGAGAGAAAGGCCATGCTGGCCACGCTGACGGGAC	1715
1020	Db	CCTGGGCGGCGGCAAGAAACGGAAAGAGAGAAAGGCCATGCTGGCCACGCTGACGGGAC	1079

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Qy 1716 TCGGGCAACTCCATGGAAGGGCTGATGCCGCGTGGGTTCTTGATCGTCTTCTCCCG 1775
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Qy 1776 GACCAAGGACTCCAAAGGCTTCGCCAGATGGGCAATGATGATTCAGAGAAAGACACCG 1835
Db 1140 GACCAAGGACTCCAAAGGCTTCGCCAGATGGGCAATGATGATTCAGAGAAAGACACCG 1199
Qy 1836 GGGCACCACAGATGCCCTGGAACCTGAGAGATGAGTGGATGAGTTCCTGAGCCGTCGCAT 1895
Db 1200 GGGCACCACAGATGCCCTGGAACCTGAGAGATGAGTGGATGAGTTCCTGAGCCGTCGCAT 1259
Qy 1896 CGATGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTCTGTCTCACCTT 1955
Db 1260 CGATGCCCGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTCTGTCTCACCTT 1319
Qy 1956 CCAGAGAGAGATTTGAGAGAAAGTACTCCCGAAGGTGGATCCCGCTTCGGAGCCTA 2015
Db 1320 CCAGAGAGAGATTTGAGAGAAAGTACTCCCGAAGGTGGATCCCGCTTCGGAGCCTA 1379
Qy 2016 CGTTGCTGTGCCCTGTGTTCTGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCC 2075
Db 1380 CGTTGCTGTGCCCTGTGTTCTGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCC 1439
Qy 2076 AACTCCACCCTGATGCTTGGGATCTATGCCAGCATCTTCTGCTGCTGCTTAATCACCGT 2135
Db 1440 AACTCCACCCTGATGCTTGGGATTTATGCCAGCATCTTCTGCTGCTGCTTAATCACCGT 1499
Qy 2136 GCTGATCTGCTGTGATCTCTGTGTTCTGTTCCCTTAAGGCCCTGCAAGCTCTGTGTC 2195
Db 1500 GCTGATCTGCTGTGATCTCTGTGTTCTGTTCCCTTAAGGCCCTGCAAGCTCTGTGTC 1559
Qy 2196 CCGCAGCATTTGCCCTCAGCGGCACATAGCACCGCATGTTGGCATCTTTTCGTCCTGCT 2255
Db 1560 CCGCAGCATTTGCCCTCAGCGGCACATAGCACCGCATGTTGGCATCTTTTCGTCCTGCT 1619
Qy 2256 TGTGTTTACTTCTGCCATTTGCCACATGTTTCACTGTAACACACACCCCCATAGGAGCTG 2315
Db 1620 TGTGTTTACTTCTGCCATTTGCCACATGTTTCACTGTAACACACACCCCCATAGGAGCTG 1679
Qy 2316 TGCAGCCCGATGCTGAATTTAATCACTGCTGATCACTGCTGCTGCCACCTGAGCAGCT 2375
Db 1680 TGCAGCCCGATGCTGAATTTAATCACTGCTGATCACTGCTGCTGCCACCTGAGCAGCT 1739
Qy 2376 CAATTACTCTCTGGGCTGATGCTCCCTGTGTGAGGGCACCATGCCACCTGCGACTT 2435
Db 1740 CAATTACTCTCTGGGCTGATGCTCCCTGTGTGAGGGCACCATGCCACCTGCGACTT 1799
Qy 2436 TCCTGAGTACTTC 2448
Db 1800 TCCTGAGGTGTT 1812
```

RESULT 12

ABS54132
ID ABS54132 standard; cDNA; 1812 BP.

AC ABS54132;

AC 20-NOV-2002 (first entry)

DE Human cDNA encoding partial Adenylyl cyclase isoform 6, AC-VI #2.

XX Human; ss; gene; adenylyl cyclase isoform 6; AC-VI; CHF; gene therapy;
KW beta-adrenergic signalling protein; congestive heart failure; cardiant;
KW cardiac function; adenovirus vector; transgenic; gene therapy;
KW beta-adrenergic signalling protein; beta-ASP; heart disease.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1812

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/product= "Partial adenylyl cyclase isoform 6"
/partial
/note= "No start or stop codon shown"

US2002103147-A1.

01-AUG-2002.

26-DEC-2000; 2000US-0750240.

27-DEC-1999; 99US-0472667.

(HAMM/) HAMMOND H K.

(INSE/) INSEL P A.

(PING/) PING P.

(POST/) POST S R.

(GAOM/) GAO M.

Hammond HK, Insel PA, Ping P, Post SR, Gao M;

WPI; 2002-690626/74.

P-PSDB; ABG32867.

Enhancing cardiac function in a mammal for treating heart disease such as congestive heart failure, by delivering to the heart of the mammal a vector comprising a gene encoding a beta-adrenergic signalling protein

Claim 75; Page 34-35; 69pp; English.

The invention relates to enhancing cardiac function in a mammal, involves delivering a vector to the heart of the mammal, where the vector comprises a gene encoding a beta-adrenergic signalling protein (beta-ASP) e.g. adenylyl cyclase isoform 6 (AC-VI) operably linked to a promoter. Generating a recombinant replication-defective viral particle involves introducing first and second plasmids into a replication-permissive mammalian cell expressing one or more adenovirus genes conferring replication competence, where the first plasmid comprises a gene encoding a beta-ASP operably linked to a promoter and further gene encoding a replication-defective human adenovirus genome, and the second plasmid comprises a replication-proficient human adenovirus genome and further comprises an additional polynucleotide sequence making the second plasmid too large to be encapsidated in an adenovirus particle, where rescue recombination takes place between the first plasmid and the second plasmid to generate a recombinant adenoviral genome comprising the gene encoding a beta-ASP but lacking one or more adenoviral replication genes, where the recombinant genome is sufficiently small to be encapsidated in an adenovirus particle, identifying successful recombinant viral vectors in cell culture, and propagating a resulting recombinant viral particle in replication-permissive mammalian cells expressing the missing adenoviral replication genes to generate a recombinant replication-defective viral particle. The method is useful for enhancing cardiac function in a mammal, preferably human and is specifically useful for treating heart diseases such as congestive heart failure (CHF). The present sequence is a partial cDNA encoding human Adenylyl cyclase isoform 6, AC-VI, a beta-ASP, used in the method of the invention.

Sequence 1812 BP; 361 A; 539 C; 507 G; 405 T; 0 other;

Query Match 49.6%; Score 1763.4; DB 24; Length 1812;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1789; Conservative 21; Indels 3; Gaps 1;

Qy 636 TTACGTGGTGTGGGATCTCTGGCGCAGTGCAGTTCGGGGCGCTCTCGCAGCAGCCC 695
Db 3 TAACGTGGTGTGGGATCTCTGGCGCAGTGCAGTTCGGGGCGCTCTCGCAGCAGCCC 62

Qy 696 GGGCAGCCCTCTGGCGGCTCTGGTCTGTTCTTTGTCTACATCGCTACACGCT 755
Db 63 GCGCAGCCCTCTGGCGGCTCTGGTCTGTTCTTTGTCTACATCGCTACACGCT 122

Qy 756 CTCTCCCATCCGCATCGGGGCTGCCGCTCTCTCAGCGGCTCTGCCACCTTGCATTT 815

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Db 123 CTTCCCATCCGATCGGGCTGCGGCTCTCTCAGCGCTGGGCTCTCCACCTTGCATTT 182
Qy 816 GATCTTGGCTGGCAACTTAAACGTTGGTGATGCTCTCTCTGGAAGCAGCTCGGTGCCAA 875
Db 183 GATCTTGGCTGGCAACTTAAACGTTGGTGATGCTCTCTCTGGAAGCAGCTCGGTGCCAA 242
Qy 876 TGTGCTGCTGTTCTCTGTGCACCAACGTCATTGGCATCTGCACACACTATFCCAGCAGAGT 935
Db 243 TGTGCTGCTGTTCTCTGTGCACCAACGTCATTAGCATCTGCACACACTATFCCAGCAGAGT 302
Qy 936 GTCTCAGCGCCAGGCTTTTCAGAGACCCCGGTTTACATCCAGGCCCGGCTCCACTGCA 995
Db 303 GTCTCAGCGCCAGGCTTTTCAGAGACCCCGGTTTACATCCAGGCCCGGCTCCACTGCA 362
Qy 996 GCATGAGAAATCGGACAGGAGCGGCTGTCTGTCTGCTGATTTGCCCGCCAGCAGTTGGCCAT 1055
Db 363 GCATGAGAAATCGGACAGGAGCGGCTGTCTGTCTGCTGATTTGCCCGCCAGCAGTTGGCCAT 422
Qy 1056 GGAGATGAAGAAGACATCAACACAAAAGAAAGACATGATGTTTCCAAAGATCTACAT 1115
Db 423 GGAGATGAAGAAGACATCAACACAAAAGAAAGACATGATGTTTCCAAAGATCTACAT 479
Qy 1116 ACAGAGCATGACATGTCAGCATCTCTGTTTGCAGACATGAGGGCTTCCAGGCTTGGC 1175
Db 480 ACAGAGCATGACATGTCAGCATCTCTGTTTGCAGACATGAGGGCTTCCAGGCTTGGC 539
Qy 1176 ATCCAGTGCTGCTGCGCAGGAGCTGTCTATGATCCCTGATGAGCTCTTTGCCCGGTTTGA 1235
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Db 1140 GACCAAGGACTCAAGGCTTCCGCGAGATGGGCTTGTGATGTTCCAGCAAGAGAGAGAGAGAGAGAG 1199
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Db 1200 GGGCACCCCAAGATGCCCTTGAAACCTTGAGGATGAGTGGATGAGTTCTTGAGCGCGTGGCCAT 1259
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Db 1260 CGATGCCCGCAGCATTGATCAGCTGCGGAAGAGACCATGTGCGCGGTTTCTGCTCACCTT 1319
Qy 1956 CCAGAGAGAGATCTTGAGAAAGATCTCCCGGAAGTGGATCCCCGCTTGGAGCCTA 2015
Db 1320 CCAGAGAGAGATCTTGAGAAAGATCTCCCGGAAGTGGATCCCCGCTTGGAGCCTA 1379
Qy 2016 CGTTGCCCTGCGGCTGTTGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2075
Db 1380 CGTTGCCCTGCGGCTGTTGGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1439
Qy 2076 ACATCCACCCCTGATGCTTGGGATCTATGCCAGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2135
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Qy 2136 GCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2195
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Db 1740 CAATTAATCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1799
Qy 2436 TCCTGAGTACTT 2448
Db 1800 TCCTGAGTACTT 1812

RESULT 13
AAV23246
ID AAV23246 standard; cDNA; 2127 BP.
XX AC AAV23246;
XX AC
XX DT 17-JUL-1998 (first entry)
XX DE Human adenylylase isoform VI encoding cDNA.
XX KW Human; adenylylase VI; AC-VI; beta-adrenergic signalling protein;
transgene; gene therapy; congestive heart failure; cardiac function;
adenovirus; ss.
XX OS Homo sapiens.
XX FH Key
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FT /note= "no stop codon given; Xaa = unknown"
FT misc_difference 315
FT /*tag= b
FT /note= "n indicates a gap of about 0.5 kb"
XX PN W09810085-A2.
XX XX 12-MAR-1998.
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1582 GGTCCCGAGTGCACTGCACAGGAAGTGGTCAATGACCTCAACAGAGCTCTTTCGCGCGGTTT 1641
1234 GACAAGCTGGCTGGGAGAAATCACTGCTCAGGATCAAGATCTTGGGGGACTGTATTAC 1293
1642 GACAAGCTGGCGCAGAGAAATCACTGTTACGTATTAAAGATCCTTGGGGATGTTATTAC 1701
1294 TGTGTGTCAGGGCTGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1353
1702 TGGCTCTCGGGGCTGCTGAGCAAGGGGCTGACCAAGGCTGCTGCTGCTGCTGCTGCTGCT 1761
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RESULT 15
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AC AAQ95540;
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DT 31-JAN-1996 (first entry)
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KW Cardiac adenylyl cyclase; effector enzyme; ss.
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OS Homo sapiens.
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FH Key Location/Qualifiers
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FT FT /*tag= a
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PD 21-MAR-1995.
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PF 02-JUL-1992; 92TW-0105242.
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PR 12-JUN-1992; 92US-0899068.
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PA (AMCY) AMERICAN CYANAMID CO.
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DR WPI; 1995-214006/28.
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DR P-PSDB; AAR78519.
XX
PT Cardiac adenylyl cyclase and corresp. DNA - having specified
PS sequences
PS Claim 1; Fig 2; 45pp; Chinese.
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CC AAQ95540 encodes AAR78519, the novel effector enzyme cardiac adenylyl
CC cyclase.
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SQ Sequence 4356 BP; 836 A; 1372 C; 1373 G; 775 T; 0 other;

Query Match 49.3%; Score 1750.8; DB 16; Length 4356;
Best Local Similarity 72.3%; Pred. No. 0;
Matches 2330; Conservative 0; Mismatches 876; Indels 17; Gaps 4;

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[illegible]

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Db	3528	TGTGGCCAGCCGATGGACAGCACCGCGGTGCGGAGCCGATCCAGGTCAACACGAGCAT	3587
QY	3396	GTACCAAGTTCTAGCTGCCAAGGCTACCAAGCTGGAGTGTGAGGGGTGTGTCAGAGTGAA	3455
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QY	3456	GGGCAAGGGGAGATGACCACTTCTTCTCAATTTGGGGGGCCCC	3498
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Search completed: January 7, 2004, 02:08:27
Job time : 934 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: January 6, 2004, 23:23:50 ; Search time 12714 Seconds
(without alignments)
11429.211 Million cell updates/sec

Title: US-09-750-240-10
Perfect score: 3552
Sequence: 1 atgcacgttgtagtgccct.....aaggaccacagtggtggcact 3552

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
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- 10: gb_ro.*
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- 12: gb_sy.*
- 13: gb_un.*
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- 32: em_htg_other.*
- 33: em_htg_mus.*
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- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3552	100.0	3552	6	AX189766	AX189766 Sequence
2	3545.6	99.8	4942	6	AR236745	AR236745 Sequence
3	3545.6	99.8	6463	9	AF250226	AF250226 Homo sapi
4	3484.8	98.1	3549	6	AR174473	AR174473 Sequence
5	3484.8	98.1	3549	6	AX189761	AX189761 Sequence
6	3443.2	96.9	3582	6	AX189768	AX189768 Sequence
7	3220.8	90.7	5877	9	AB007882	AB007882 Homo sapi
8	3057.6	86.1	4046	4	DOGADENCCYC	M94968 Canis faml
9	3051.2	85.9	4046	6	I29958	I29958 Sequence 1
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11	2816.2	79.3	5841	10	MUSADCCYC	M93422 Mouse adeny
12	2810.4	79.1	4131	6	AR106659	AR106659 Sequence
13	2810.4	79.1	4131	10	RATADCCYC	M96160 Rattus norv
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15	2785.2	78.4	3465	10	MUSADNLCCYC	M96653 Mus musculu
16	1763.4	49.6	1812	6	AR174472	AR174472 Sequence
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18	1761	49.6	4523	6	BD135829	BD135829 Cloning a
19	1752	49.3	4545	4	DOGADNCCYC	M88649 Canis faml
20	1739.6	49.0	4995	4	OCMRADCCYC	Z29371 O.cuniculus
21	1703.2	48.0	4847	10	RATADCCYC	M96159 Rattus norv
22	1696.2	47.8	3924	6	AR106658	AR106658 Sequence
23	1523.4	42.9	2743	9	AF497517	AF497517 Homo sapi
24	1479.6	41.7	4236	5	GGA293817	AJ293817 Gallus ga
25	1304.4	36.7	4401	10	BC035550	BC035550 Mus muscu
26	924	26.0	3963	10	AK122279	AK122279 Mus muscu
27	886.2	24.9	3137	6	AX418303	AX418303 Sequence
28	883.4	24.9	2554	9	AK093840	AK093840 Homo sapi
29	867.4	24.4	144383	9	AC117498	AC117498 Homo sapi
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31	841.8	23.7	2429	4	DOGADCCYC	M97886 Canis faml
32	612.8	17.3	184182	2	AC129405	AC129405 Rattus no
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34	612.8	17.3	250885	2	AC113161	AC113161 Rattus no
35	610.2	17.2	139619	2	AC074028	AC074028 Mus muscu
36	610.2	17.2	235982	2	AC138221	AC138221 Mus muscu
37	604.4	17.0	3978	4	BOVADC	M25579 Bovine aden
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ALIGNMENTS

RESULT 1
AX189766
LOCUS AX189766 3552 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 10 from Patent WO0148164.
ACCESSION AX189766
VERSION AX189766.1 GI:15143139
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Hammond, H.K. and Gao, M.
AUTHORS Gene therapy for congestive heart failure
TITLE Patent: WO 0148164-A 10 05-JUL-2001;
JOURNAL

THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)

FEATURES		Location/Qualifiers		Score		DB		Length		3552;		DB		Length		3552;			
source		1..3552		/organism="Homo sapiens"		100.0%;		Pred. No. 0;		Matches 3552;		Conservative 0;		Mismatches 0;		Indels 0;		Gaps 0;	
BASE COUNT		686 a 1037 c 1068 g 761 t																	
ORIGIN																			
Qy	1	ATGTCATGGTTT	100.0%;	Score 3552;	DB 6;	Length 3552;													
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Qy	781	GTCTCAGCGCT	100.0%;																
Db	781	GTCTCAGCGCT	100.0%;																
Qy	841	GGTGATGCTTC	100.0%;																
Db	841	GGTGATGCTTC	100.0%;																

Qy	901	GTCAATTGGCAT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	901	GTCAATTGGCAT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	961	ACCGCGGTTAT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	961	ACCGCGGTTAT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1021	CTGCTGCTGCT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1021	CTGCTGCTGCT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1081	AAAAAAGAACAT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1081	AAAAAAGAACAT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1141	CTGTTTGCAGAT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1141	CTGTTTGCAGAT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1201	GTCAATGACCT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1201	GTCAATGACCT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1261	CTGAGGATCAAG	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1261	CTGAGGATCAAG	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1321	GCAGCAATGCT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1321	GCAGCAATGCT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1381	GTACGTGAGTG	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1381	GTACGTGAGTG	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1441	CACTGCGGGCT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1441	CACTGCGGGCT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1501	CTGGCCAAACCA	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1501	CTGGCCAAACCA	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1561	CTSCAGTACTGA	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1561	CTSCAGTACTGA	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1621	TACCTCAAGGAG	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1621	TACCTCAAGGAG	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1681	GAGGAGAGGCCA	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1681	GAGGAGAGGCCA	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1741	ATGCGCGCTGCT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1741	ATGCGCGCTGCT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1801	CAGATGGGCATT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1801	CAGATGGGCATT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1861	GAGGATGAGTGA	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1861	GAGGATGAGTGA	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1921	CGGAAGCACTGT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1921	CGGAAGCACTGT	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Qy	1981	TACTCCCGGAAG	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;
Db	1981	TACTCCCGGAAG	100.0%;	0;	100.0%;	0;	100.0%;	0;	100.0%;	0;

1981 TACTCCCGAAGGTGGATCCCGCTTCGGAGCTACGTTGCTGTGCCTGTGTGCTCTTC 2040
2041 TGCTTCATCTGCTTCATCAGCTTCTCATCTTCCACACATCCACCTCATGCTTGGGATC 2100
2041 TGCTTCATCTGCTTCATCAGCTTCTCATCTTCCACACATCCACCTCATGCTTGGGATC 2100
2101 TATGCCAGATCTTCTGCTGCTGCTTAATACCGTGTGATCTGCTGTGCTGTGCTGTG 2160
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2161 GGTTCCTCTGTTCCCTAAGSCCTGCAACGCTGTGCTCCCGCAGCATGTCGCTCAGGGCA 2220
2161 GGTTCCTCTGTTCCCTAAGSCCTGCAACGCTGTGCTCCCGCAGCATGTCGCTCAGGGCA 2220
2221 CATAGCAGCGAGTTGGCATCTTTTCCGTCCTGCTGTGTTTACTTCTGCGCATGCGCAAC 2280
2221 CATAGCAGCGAGTTGGCATCTTTTCCGTCCTGCTGTGTTTACTTCTGCGCATGCGCAAC 2280
2281 ATGTTTCACTGTAAACACACACCCCATACGGAGCTGTGAGCCGGATGCTGAATTTAAACA 2340
2281 ATGTTTCACTGTAAACACACACCCCATACGGAGCTGTGAGCCGGATGCTGAATTTAAACA 2340
2341 CCTGTGATCATCACTGCTGCGACCTGCGACCTGAGCTCAATTACTCTCTGGGCTGATGCT 2400
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2401 CCCCTGTGTAGGGGACCATGCGCCACCTGCGAGCTTCTCTGAGTACTTCTATCGGGAACATG 2460
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2461 CTGCTGAGTCTCTTGGCCAGCTCTGCTTCTCTGACATCAGCAGCATCGGGAAGTTGGCC 2520
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2581 ATCTTTGACAACTATGACTACTGCTTGGCGTCCATGCTTGGCTTCTTCCATGAGACC 2640
2641 TTTGATGGCTGGACTGCTCCAGCTGCAAGGAGGTGGCCCTCAATATATGACCCCTGTG 2700
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2701 ATTCTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
2701 ATTCTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
2761 CGCCTAGACTTCTCTGGAACCTACAGGCAACAGGGGAGAGGAGATGGAGGAGCTA 2820
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2821 CAGGCATACACCGAGGCTGCTGATCAATCTTCTGCCCAAGAGCTGCGGCCCACTTC 2880
2881 CTGGCCCGGAGCGCGCAATGATGATCTACTATCACTATGCTGCTGCTGCTGCTGCTGCT 2940
2881 CTGGCCCGGAGCGCGCAATGATGATCTACTATCACTATGCTGCTGCTGCTGCTGCTGCT 2940
2941 ATGTTTGTCTCATGTCCTCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
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3001 GGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
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3061 GAGGAGCGGTTCGCGCAGCTGGAAGAATCAAGACGATGCTGCTGCTGCTGCTGCTGCTGCT 3120

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3121 TCAGGGCTGAACGCGCAGCAGCTACGATCAGGTGGCGCGCTCCACATCACTGCTGCTGCT 3180
3121 TCAGGGCTGAACGCGCAGCAGCTACGATCAGGTGGCGCGCTCCACATCACTGCTGCTGCT 3180
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3361 GGGTCCCGGACCGAATCCAGGTGACCGACCTGTACAGGTCTTAGTCTGACAGGCTTAC 3420
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3421 TACCAGCTGGAGTGTGAGGGGTGCTGAGGTGAAGGCAAGGGGAGATGACACCTTAC 3480
3481 TTCTCTAATGGGGGCGCCAGCAGTAAACAGGGCCAGCAGCAAAATTCAGCTGAAGGAGC 3540
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3541 AAGGTGGGCACT 3552
3541 AAGGTGGGCACT 3552

RESULT 2
AR236745
LOCUS AR236745 4942 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6465237.
ACCESSION AR236745
VERSION AR236745.1 GI:27280909
KEYWORDS SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 4942)
AUTHORS Tomlinson, J.E.
TITLE Cloning and characterization of a human adenylyl cyclase
JOURNAL Patent: US 6465237-A 1 15-OCT-2002;
FEATURES Location/Qualifiers
1..4942
source /organism="unknown"
BASE COUNT 953 a 1404 c 1512 g 1073 t
ORIGIN

Query Match 99.8%; Score 3545.6; DB 6; Length 4942;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3548; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGTCATGTTTATGTCCTCTGCTGCTTAAAGTGAATGAACGGAACAGCTTGGGGT 60
Db 145 ATGTCATGTTTATGTCCTCTGCTGCTTAAAGTGAATGAACGGAACAGCTTGGGGT 204
Qy 61 GAACGCAATGGCAGAGAGCGTTCCGGCGCGCTGGCACTCGGCGAGGTGGCTTCTGCACG 120
Db 205 GAACGCAATGGCAGAGAGCGTTCCGGCGCGCTGGCACTCGGCGAGGTGGCTTCTGCACG 264
Qy 121 CCCGCTATATGAGTGTCTCCGGGATGACAGACACCCAGCCCGCCACCTTCCGGGCCCC 180
Db 265 CCCGCTATATGAGTGTCTCCGGGATGACAGACACCCAGCCCGCCACCTTCCGGGCCCC 324
Qy 181 CCTCGGTCCCTGGCAGGATGACGCTTATCCGGAGGGCGGCCACAGGCAAGGGCAAG 240

Db 325 CCTCGTGCCCTTGGCAGGATGACGCTTCATCCGGAGGGCGCCAGGCAAG 384
QY 241 GAGCTGGGGCTGGGGCAGTGGCCCTGGGGCTTCGAGGATACCGAGGTGACAAACGACAGCG 300
Db 385 GAGCTGGGGCTGGGGCAGTGGCCCTGGGGCTTCGAGGATACCGAGGTGACAAACGACAGCG 444
QY 301 GGGGGGACGGCTGAGGTGGGGCGCCGACGCGGTGCCAGAGTGGAGATCCTGCTGGCG 360
Db 445 GGGGGGACGGCTGAGGTGGGGCGCCGACGCGGTGCCAGAGTGGAGATCCTGCTGGCG 504
QY 361 CGTCTGGTGAGGTGTTCCAGTGAAGCAGTTCGGTTCGGCCCAAGCTGGAGCGGCTGTAT 420
Db 505 CGTCTGGTGAGGTGTTCCAGTGAAGCAGTTCGGTTCGGCCCAAGCTGGAGCACCTGTAT 564
QY 421 CAGCGGTACTTCTCCAGATGAACAGAGCAGCTGACGCTGTGATGGGGGCTGTGGTG 480
Db 565 CAGCGGTACTTCTCCAGATGAACAGAGCAGCTGACGCTGTGATGGGGGCTGTGGTG 624
QY 481 CTGCTCACAGCGGTGCTGGCTTTCACGCGCGCACCCGCGCCCTCAGCCCTGCTAT 540
Db 625 CTGCTCACAGCGGTGCTGGCTTTCACGCGCGCACCCGCGCCCTCAGCCCTGCTAT 684
QY 541 GTGGCACTGTGGCGCTGGCGCGCCCTGTTGTGGGGCTCATGTGTGTGTAAACCG 600
Db 685 GTGGCACTGTGGCGCTGGCGCGCCCTGTTGTGGGGCTCATGTGTGTGTAAACCG 744
QY 601 CATAGCTTCCGCCAGGACTCCATGTGGGTGAGTTCAGTGTGTGGGCTGCTGGCG 660
Db 745 CATAGCTTCCGCCAGGACTCCATGTGGGTGAGTTCAGTGTGTGGGCTGCTGGCG 804
QY 661 GCAGTGCAGTTCGGGGCGCTCTCGCAGCAGACCCGCGCAGCCCTCTCGCGGCTCTGG 720
Db 805 GCAGTGCAGTTCGGGGCGCTCTCGCAGCAGACCCGCGCAGCCCTCTCGCGGCTCTGG 864
QY 721 TGCCCTGTGTTTGTGTACATGCGCTACAAGCTTCTCCCATTCGCAATGCGGGTGC 780
Db 865 TGCCCTGTGTTTGTGTACATGCGCTACAAGCTTCTCCCATTCGCAATGCGGGTGC 924
QY 781 GTCTCAGCGGCTGGGCTCTCCAGCTTCATTTGATCTTGGCTGGCACTTAACCGT 840
Db 925 GTCTCAGCGGCTGGGCTCTCCAGCTTCATTTGATCTTGGCTGGCACTTAACCGT 984
QY 841 GGTGATGCTCTCTTGGAGCAGCTCGTGCCAAATGTGCTGTCTCTCTGCAACCAAC 900
Db 985 GGTGATGCTCTCTTGGAGCAGCTCGTGCCAAATGTGCTGTCTCTCTGCAACCAAC 1044
QY 901 GTCAATGGGATCTGCAACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAAGAG 960
Db 1045 GTCAATGGGATCTGCAACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAAGAG 1104
QY 961 ACCCGGTTTACATCCAGGCGCCGCTCCAGCTCAGCATCAGAAATCGGACAGGAGCGG 1020
Db 1105 ACCCGGTTTACATCCAGGCGCCGCTCCAGCTCAGCATCAGAAATCGGACAGGAGCGG 1164
QY 1021 CTGCTGCTGTCGTTATTTGCCCGCAGCAGCTTGGCCATGGAGATGAAGAAGACATCAACACA 1080
Db 1165 CTGCTGCTGTCGTTATTTGCCCGCAGCAGCTTGGCCATGGAGATGAAGAAGACATCAACACA 1224
QY 1081 AAAAAAGAACATGATGTTTCCACAGATCTACATCAGAAAGCATGCAATGTCAAGATC 1140
Db 1225 AAAAAAGAACATGATGTTTCCACAGATCTACATCAGAAAGCATGCAATGTCAAGATC 1284
QY 1141 CTGTTTGCAGACATGAGGCTTCCAGGCTGGCATCCAGTGCATCCAGTGCATCCAGGAGCTG 1200
Db 1285 CTGTTTGCAGACATGAGGCTTCCAGGCTGGCATCCAGTGCATCCAGTGCATCCAGGAGCTG 1344
QY 1201 GTCATGACCCCTGAATGAGCTTCTTGGCCCGTGTGACAAAGCTGGCTGGAGAAATCACTGC 1260
Db 1345 GTCATGACCCCTGAATGAGCTTCTTGGCCCGTGTGACAAAGCTGGCTGGAGAAATCACTGC 1404
QY 1261 CTGAGGATCAAGATCTTGGGGGACTGTACTACTGTGTGTCAGGCTGCGCGAGGCGCGG 1320
Db 1405 CTGAGGATCAAGATCTTGGGGGACTGTACTACTGTGTGTCAGGCTGCGCGAGGCGCGG 1464

QY 1321 GCCGACCATGCCCATCTGTGTGGAGATGGGGGTAGACATGATGAGGCCATCTCGCTG 1380
Db 1465 GCCGACCATGCCCATCTGTGTGTGGAGATGGGGGTAGACATGATGAGGCCATCTCGCTG 1524
QY 1381 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGTG 1440
Db 1525 GTACGTGAGGTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGCGCGTG 1584
QY 1441 CACTGCGGCGTCTTGGCTTGGGAAATGGCAGTTTCGATGTGTGGTCCATGATGTGACC 1500
Db 1585 CACTGCGGCGTCTTGGCTTGGGAAATGGCAGTTTCGATGTGTGGTCCATGATGTGACC 1644
QY 1501 CTGGCCAAACCATGAGGAGGAGGCGCGGCTGGCGCATCCACATCACTCTCGGGCAACA 1560
Db 1645 CTGGCCAAACCATGAGGAGGAGGCGCGGCTGGCGCATCCACATCACTCTCGGGCAACA 1704
QY 1561 CTGCACTACTGAAACGGGCACTACGAGGTGGAGCCAGGGCGTGGTGGCGAGCGCAACGCG 1620
Db 1705 CTGCACTACTGAAACGGGCACTACGAGGTGGAGCCAGGCGGTGGTGGCGAGCGCAACGCG 1764
QY 1621 TACCTCAAGGAGGAGCAGCATTTGAGACTTTTCTCATCTGGGCGCGCAGCCAGAAACGGAAA 1680
Db 1765 TACCTCAAGGAGGAGCAGCATTTGAGACTTTTCTCATCTGGGCGCGCAGCCAGAAACGGAAA 1824
QY 1681 GAGGAGAGGCGCATGTGCGCAAGCTGACGCGGACTCGGGCCAACTCCATGGAAGGCGTG 1740
Db 1825 GAGGAGAGGCGCATGTGCGCAAGCTGACGCGGACTCGGGCCAACTCCATGGAAGGCGTG 1884
QY 1741 ATGCCGCGTGGGTTCCTGATCGTGCCTTCTCCCGAACCAAGGACTCCAAAGGCTTCCGC 1800
Db 1885 ATGCCGCGTGGGTTCCTGATCGTGCCTTCTCCCGAACCAAGGACTCCAAAGGCTTCCGC 1944
QY 1801 CAGATGGGCAATGATGATTCAGCAAAAGACAACCGGGCGCACCAAGATGCCCCCTGAACCT 1860
Db 1945 CAGATGGGCAATGATGATTCAGCAAAAGACAACCGGGCGCACCAAGATGCCCCCTGAACCT 2004
QY 1861 GAGGATGAGGTGATGAGTCTTCTGAGCGGTGCGCATCGATGCCCGCAGCATTTGATCAGCTG 1920
Db 2005 GAGGATGAGGTGATGAGTCTTCTGAGCGGTGCGCATCGATGCCCGCAGCATTTGATCAGCTG 2064
QY 1921 CGGAAGGACCATGTGCGCGGTTTCTGCTCACCTTCCAGAGAGAGGATCTTGAGAGAGAG 1980
Db 2065 CGGAAGGACCATGTGCGCGGTTTCTGCTCACCTTCCAGAGAGAGGATCTTGAGAGAGAG 2124
QY 1981 TACTCCCGAAGGTGATCCCGCTTCGGAGCCTAGTTCCTGCTGCTGCTGCTGCTGCTGCTTTC 2040
Db 2125 TACTCCCGAAGGTGATCCCGCTTCGGAGCCTAGTTCCTGCTGCTGCTGCTGCTGCTTTC 2184
QY 2041 TGCTTCATCTGCTTCATCCAGCTTCTCATCTCCACACTCCACCTGATGCTTGGGATC 2100
Db 2185 TGCTTCATCTGCTTCATCCAGCTTCTCATCTCCACACTCCACCTGATGCTTGGGATC 2244
QY 2101 TATGCGAGCATCTTCTGCTGCTGCTTAAATCACCGTCTGATCTGCTGCTGCTGCTGCTGCT 2160
Db 2245 TATGCGAGCATCTTCTGCTGCTGCTTAAATCACCGTCTGATCTGCTGCTGCTGCTGCTGCT 2304
QY 2161 GGTTCCTGTTCCCTAAGGCGCTGCAACCGTCTGCTCCCGCAGCATTTGCTCGCTCACGGGCA 2220
Db 2305 GGTTCCTGTTCCCTAAGGCGCTGCAACCGTCTGCTCCCGCAGCATTTGCTCGCTCACGGGCA 2364
QY 2221 CATAGCACCGCAGTTGGCATCTTTTCCGCTCTGCTTGTGTTTACTTCTGCAATTTGCCAAC 2280
Db 2365 CATAGCACCGCAGTTGGCATCTTTTCCGCTCTGCTTGTGTTTACTTCTGCAATTTGCCAAC 2424
QY 2281 ATGTTCACTGTAAACCAACACCCCATACCGAGCTGTGCGAGCCCGGATGCTGAATTTAAACA 2340
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Db 2485 CTTGCTGACATCACTGCTGCGCACCTGACGAGCTCAATTTACTTCTCTGGGCGCTGGATGCT 2544

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Db	2545	CCCCCTGTGTGAGGGGACCATGCCACCTGCGAGCTTTCTCTGAGTACTTTCATCGGGAAACATG	2604
Qy	2461	CTGCTGAGTCTCTTTGGGCAGCTCTGTCTTCTCTGCACATCAGCAGCATCGGGAGTTGGCC	2520
Db	2605	CTGCTGAGTCTCTTTGGGCAGCTCTGTCTTCTCTGCACATCAGCAGCATCGGGAGTTGGCC	2664
Qy	2521	ATGATCTTTGTCTTTGGGGCTCATCTATTTTGGTGTCTGCTTCTGTCTGGGTCCCCCAGCCACC	2580
Db	2665	ATGATCTTTGTCTTTGGGGCTCATCTATTTTGGTGTCTGCTTCTGTCTGGGTCCCCCAGCCACC	2724
Qy	2581	ATCTTTGACAACTATGACCTACTGCTTTGGGTCATGCGCTTGGCTTCTTCCAATGAGAGCC	2640
Db	2725	ATCTTTGACAACTATGACCTACTGCTTTGGGTCATGCGCTTGGCTTCTTCCAATGAGAGCC	2784
Qy	2641	TTTGATGGGCTGGACTGTCAGCTGTCAGGGAGGGTGCCCTCAAATATATGACCCCTGTG	2700
Db	2785	TTTGATGGGCTGGACTGTCAGCTGTCAGGGAGGGTGCCCTCAAATATATGACCCCTGTG	2844
Qy	2701	ATTCTGCTGGTTTTGGGCTGGCGCTGTATCTGCACTCTCAGCAGGTGGAGTCGACTGCC	2760
Db	2845	ATTCTGCTGGTTTTGGGCTGGCGCTGTATCTGCACTCTCAGCAGGTGGAGTCGACTGCC	2904
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Qy	2821	CAGGCATACACGGAGGCTGCTGCATTAACAATTTCTGCCCAAGGACGTGGCGGCCCACTTC	2880
Db	2965	CAGGCATACACGGAGGCTGCTGCATTAACAATTTCTGCCCAAGGACGTGGCGGCCCACTTC	3024
Qy	2881	CTGGCCCGGAGCGCCCAATGATGAATCTTACTATCAGTCTGTGAGTGTGTGGCTGTT	2940
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Db	3085	ATGTTTGCTCCTCATPTGCAACTTCTCTCGAGTTCTATGTGAGCTGGAGGCAACAATGAG	3144
Qy	3001	GGTGTCCAGTGCCTGGCGTCTCAACGAGATCATCGCTGACTTTGTAGATGATTAATCAGC	3060
Db	3145	GGTGTCCAGTGCCTGGCGTCTCAACGAGATCATCGCTGACTTTGTAGATGATTAATCAGC	3204
Qy	3061	GAGGAGCGGTTCCGCGAGCTGGAAAAGATCAAGACGATTGGTAGCACTTACATGGCTGCC	3120
Db	3205	GAGGAGCGGTTCCGCGAGCTGGAAAAGATCAAGACGATTGGTAGCACTTACATGGCTGCC	3264
Qy	3121	TCAGGGCTGAACGCCAGCACTTACGATCAGGTGGGCCGCTCCCAATCATCTGCCCTGGCT	3180
Db	3265	TCAGGGCTGAACGCCAGCACTTACGATCAGGTGGGCCGCTCCCAATCATCTGCCCTGGCT	3324
Qy	3181	GACTACGCCCATGCGGCTCATGGAGCAGATGAGCAGATCAATGAGCACTCTTTCACAAT	3240
Db	3325	GACTACGCCCATGCGGCTCATGGAGCAGATGAGCAGATCAATGAGCACTCTTTCACAAT	3384
Qy	3241	TTCCAGATGAAGATTGGGCTGAACAATGGGCCCACTCGTGGCAGGTGTCTCGGGGCTCGG	3300
Db	3385	TTCCAGATGAAGATTGGGCTGAACAATGGGCCCACTCGTGGCAGGTGTCTCGGGGCTCGG	3444
Qy	3301	AAGCCACAGTATGACATCTGGGGGAACAAGTGAATGTCTCTAGTCGTATGGCAGCAGCAGC	3360
Db	3445	AAGCCACAGTATGACATCTGGGGGAACAAGTGAATGTCTCTAGTCGTATGGCAGCAGCAGC	3504
Qy	3361	GGGGTCCCGACCGAATCCAGGTGACACCGGACCTGTATCCAGGTTCTAGCTGCCAAGGGC	3420
Db	3505	GGGGTCCCGACCGAATCCAGGTGACACCGGACCTGTATCCAGGTTCTAGCTGCCAAGGGC	3564
Qy	3421	TACCAGCTGGAGTGTCCAGGGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACTTAC	3480
Db	3565	TACCAGCTGGAGTGTCCAGGGGGTGGTCAAGGTGAAGGGCAAGGGGGAGATGACCACTTAC	3624
Qy	3481	TTCTCTAATGGGGGGCCCGACAGTTTAACAGGGGCCCGACCAAAATTCAGCTGAAGGGAGCC	3540

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Db      3625 TTCTCTAATGGGGCCCCAGCAGTTAACAGGGGCCAGCCACAAATTCAGCTGAAGGGACC 3684
Qy      3541 AAGGTGGGCACT 3552
Db      3685 AAGGTGGGCATT 3696

RESULT 3
AF250226
LOCUS   Homo sapiens adenylyl cyclase type VI mRNA, complete cds.
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 6463)
AUTHORS
Wicker, R., Catalan, A.G., Caillex, A., Starenki, D., Stengel, D.,
Sarasin, A. and Suarez, H.G.
TITLE
Cloning and expression of human adenylyl cyclase type VI in normal
thyroid tissues
JOURNAL
Biochim. Biophys. Acta 1493 (1-2), 279-283 (2000)
MEDLINE
20435313
PUBMED
10978539
REFERENCE
2 (bases 1 to 6463)
AUTHORS
Wicker, R., Gascon Catalan, A., Caillex, A.-F., Starenki, D.,
Stengel, D., Sarasin, A. and Suarez, H.G.
TITLE
Direct Submission
JOURNAL
Submitted (28-MAR-2000) Lab Etude des Relations - Instabilite
genetique et Cancer UPR 2169, Institut de Recherches sur le Cancer
CNRS-IFR 1221, 7 rue Guy Moquet, Villejuif 94801, France
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Ishikawa, K., Nagase, T., Nakajima, D., Seki, N., Ohira, M.,
Miyaajima, N., Tanaka, A., Kotani, H., Nomura, N. and Ohara, O.
TITLE Prediction of the coding sequences of unidentified human genes.
VIII. 78 new cDNA clones from brain which code for large proteins
in vitro
JOURNAL DNA Res. 4 (5), 307-313 (1997)
MEDLINE 9811655
PUBMED 9455477
REFERENCE 2 (bases 1 to 5877)
AUTHORS Ohara, O.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology, Yana 1532-3, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
COMMENT On May 9, 2002 this sequence version replaced gi:2887418.
Sequence updated (05-Jan-1998).
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VERSION M94968.1 GI:163896
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1 (bases 1 to 4046)
Katsushika, S., Chen, L., Kawabe, J., Nilakantan, R., Halnon, N.J.,
Honey, C.J., and Ishikawa, Y.
REFERENCE Cloning and characterization of a sixth adenylyl cyclase isoform:
AUTHORS types V and VI constitute a subgroup within the mammalian adenylyl
TITLE cyclase family

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (18), 8774-8778 (1992)
MEDLINE 92409599
PUBMED 1528892
COMMENT source text: Canis familiaris cardiac muscle cDNA to mRNA.
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VERSION I29958.1 GI:1820749
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4046)
AUTHORS Ishikawa,Y.
TITLE Cloning and characterization of a cardiac adenylyl cyclase
JOURNAL Patent: US 5578481-A 1 26-NOV-1996;
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DEFINITION Sequence 716 from Patent WO0188188.
ACCESSION AX305965
VERSION AX305965.1 GI:17645322
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Ishikawa, K., Asai, S., Takahashi, Y., Nagata, T. and Ishii, Y.
TITLE Method for examining ischemic conditions
JOURNAL Patent: WO 0188188-A 716 22-NOV-2001;
School Juridical Person Nihon University (JP)
FEATURES
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BASE COUNT 1214 a 1558 c 1673 g 1396 t
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Query Match 79.3%; Score 2816.2; DB 6; Length 5841;
Best Local Similarity 87.8%; Pred. No. 0;
Matches 3120; Conservative 0; Mismatches 423; Indels 10; Gaps 4;

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ACCESSION M93422
VERSION M93422.1 GI:191690
KEYWORDS adenylyl cyclase; adenylyl cyclase type VI.
SOURCE Mus musculus (house mouse)
ORGANISM Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 5841)
AUTHORS Yoshimura,M. and Cooper,D.M.
TITLE Cloning and expression of a Ca(2+)-inhibitable adenylyl cyclase
from NCB-20 cells
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (15), 6716-6720 (1992)
MEDLINE 92357702
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Query Match 79.3%; Score 2816.2; DB 10; Length 5841;
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RESULT 12
AR106659
LOCUS

Accession	Size	Type	Library
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PAT 14-FEB-2001			

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Qy 2461 CTGCTGAGTCTTGGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
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Db 3050 GGGTGGAGTGTCTGCGACTGCTCAATGAGATCATCGCGACTTTTGATGAGATCATCAGT 3109
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RESULT 13
LOCUS RATADCVB 4131 bp mRNA linear ROD 27-APR-1993
DEFINITION Rattus norvegicus adenylyl cyclase type VI mRNA, complete cds.
ACCESSION M96160
VERSION M96160.1 GI:202718
KEYWORDS adenylyl cyclase; adenylyl cyclase type VI.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 4131)
Premont,R.T.
ADENYLYL CYCLASES UNDERLYING DESENSITIZATION OF THE LIVER
ADENYLYL CYCLASE SYSTEM. STRUCTURE AND CAMP REGULATION OF LIVER
ADENYLYL CYCLASES
Thesis (1992)
REFERENCE 2 (bases 1 to 4131)
Premont,R.T., Chen,J., Ma,H.W., Ponnappalli,M. and Iyengar,R.
Two members of a widely expressed subfamily of hormone-stimulated
adenylyl cyclases
Proc. Natl. Acad. Sci. U.S.A. 89 (20), 9809-9813 (1992)
JOURNAL MEDLINE 93028552
PUBMED 1409703
COMMENT Original source text: Rattus norvegicus (strain Sprague-Dawley)
adult liver, kidney, heart cDNA to mRNA.
Location/Qualifiers
1. .4131
/organism="Rattus norvegicus"

Query Match	79.1%; Score 2810.4; DB 10; Length 4131;
Best Local Similarity	87.5%; Pred. No. 0;
Matches 3110; Conservative	0; Mismatches 436; Indels 8; Gaps 3;
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RESULT 14

RATADC
LOCUS
DEFINITION Rattus norvegicus adenylyl cyclase type VI mRNA linear ROD 12-AUG-1994
ACCESSION L01115
VERSION L01115.1 GI:202712
KEYWORDS adenylyl cyclase; adenylyl cyclase; adenylyl cyclase type VI.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 6036)
AUTHORS Krupinski J., Lehman, T.C., Frankenfield, C.D., Zwaagstra, J.C. and Watson, P.A.

TITLE Molecular diversity in the adenylyl cyclase family. Evidence for eight forms of the enzyme and cloning of type VI

JOURNAL J. Biol. Chem. 267 (34), 24858-24862 (1992)

MEADLINE 93077589

PUBMED 1332969

COMMENT Original source text: Rattus norvegicus hepatoma cDNA to mRNA.

FEATURES Location/Qualifiers

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polyA_site

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BASE COUNT

ORIGIN

Query Match 78.9%; Score 2802.4; DB 10; Length 6036;

Best Local Similarity 87.4%; Pred. No. 0;

Matches 3105; Conservative 0; Mismatches 441; Indels 8; Gaps 3;

3;

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QY	1441	CACGTGGCGCTCTTGGCTTGCAGAAATGCGAGTTGAGTGTGGTCCAAATGATGTGACC	1500
DB	1633	CACGTGGCGTCTCTTGGCTTGCAGAAATGCGAGTTGAGTGTGGTCCAAATGATGTGACC	1692
QY	1501	CTGGCCAAACACATGAGAGGACAGAGCGCGGCTGGCGGCATCCACATCACTCGGGCAACA	1560
DB	1693	CTGGCCAAACACATGAGAGGACAGAGCGCGGCTGGCGGCATCCACATCACTCGGGCCACA	1752
QY	1561	CTGCAGTACCTGAAACGGGGACTACGAGGTGAGCCAGGCGGTGGTGGCGAGCGCAACGGC	1620
DB	1753	CTGCAGTACCTGAAACGGGGACTACGAGGTGAGCCAGGCGGTGGTGGCGAGCGCAACGGC	1812
QY	1621	TACCTCAAGGACGACCATTTGAGACTTTCTCATCTGCGGCCACAGCCAGCAAAACGGAAA	1680
DB	1813	TACCTCAAGGACGACCATTTGAGACTTTCTCATCTAGGAGCCAGCCAGCAAAACGGAAA	1872
QY	1681	GAGGAGAGCCATGCTGGCCCAAGCTGCAGCGGACTCGGGCCCAACTCCATGGAAGGCTG	1740
DB	1873	GAGGAGAGCCATGCTGGCCCAAGCTGCAGCGGACTCGGGCCCAACTCCATGGAAGGACTG	1932
QY	1741	ATGCCGCGCTGGGTTCCTGATCGTGCCTTCTCCGGACCAAGGACTCCCAAGGCTTCCGC	1800
DB	1933	ATGCCGCGCTGGGTTCCTGATCGTGCCTTCTCCGGACCAAGGACTCCCAAGGACTTCCGA	1992
QY	1801	CAGATGGGCATTGATGATTTCCAGCAAAAGAACCGGGGCCACCAAGATGCCCTGAAACCTT	1860
DB	1993	CAGATGGGCATCGATGACTTAGCAAAAGAACCGGGGGTCCCAAGATGCTCTGAAACCTT	2052
QY	1861	GAGGATGAGTGTGATGATTTCTGAGCCGTGGCATCGATCCCGCAGCATTTGATCAGCTG	1920
DB	2053	GAGGATGAGTGTGATGATTTCTGAGCCGTGGCATCGATCCCGCAGCATTTGATCAGCTG	2112
QY	1921	CGAAGGACCATGTGCGCCGTTTCTGCTCACTTCCAGAGAGAGGATCTTGAGAGAAG	1980
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DB	2233	TGCTTCACTGCTTCACTCAGCTTCTCATCTTCCACACTCCACCTCGATGCTTGGGATC	2292
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DB	2293	TATGCCAGCATCTTCTGCTGCTGCTAACTCACCGTGTGATCTGTGCTGTACTCTGCT	2352
QY	2161	GGTTCTGTTCCCTAAGGCCCTGCAACGCTGTGCTCCGACGATTTGTCGCTCACGGCA	2220
DB	2353	GGTTCTTCTTCCCAACGCCCTGACGCGCTGTCCGCGAGTATCGTCCGCTCAGGGTG	2412
QY	2221	CATAGCACCGAGTTGGCATCTTTTCGCTCGTGTGTTTACTTCTGCGCATTTGCCAAC	2280
DB	2413	CACAGCACCGCTGTGAGTCTTTTCGCTCGTGTGTTTACTTCTGCGCATTTGCCAAC	2472
QY	2281	ATGTTCACTGTAAACACACCCCATACGGAGCTGTGACGCCGATGCTGAAATTTAAACA	2340
DB	2473	ATGTTCACTGTGAGTAAACACCCCATACGGAGCTGTGACGCCGATGCTGAAATTTAAACA	2532
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QY	2401	CCCTGTGTGAGGACCATGCCCCACCTGACGCTTCTGAGTACTTTCATCGGGAAACATG	2460
DB	2593	CCCTGTGTGAGGACCATGCCCCACCTGACGCTTCTGAGTACTTTCATCGGGAGTGTG	2652

QY	2461	CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGACATCAGCAGCATCGGAAAGTTGGCC	2520
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QY	2521	ATGATCTTGTCTTGGGGCTCATCTATTTGGTGTCTGCTTGTGCGGTGCCCCAGGCACC	2580
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DB	2893	ATTCTCTCGGTGTTCGCTGGCGCTGTATCTGCATGCTCTCAGAGGTGAGTGCATGCC	2852
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QY	3121	TCAGGCTGAAACGCCAGCACCTACGATCAGGTGGCGGCTCCACATCACTGCGCTGGCT	3180
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QY	3181	GACTAGCCCATGCGGCTCATGAGCAGATGAAGCACATCAATGAGCACTCTTCAACAAT	3240
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QY	3241	TTCCAGATGAAGATTCGGGTGAAACATGGGCCCAGTCTGTCGACGGTGTCTATCGGGTCTCGG	3300
DB	3433	TTCCAGATGAAGATTCGGGTGAAACATGGGTCGCTGCTGAGCAGGTGTCTATGGGGCCCG	3492
QY	3301	AAGCCACAGTATGACATCTGGGGGAAACAGTCAATGCTCTCTAGTCTGATGGACAGCACG	3360
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QY	3361	GGGGTCCCCGACCGAATCCAGGTGACCGGACTGTACCGAGTTCTTAGCTGCCAAGGGC	3420
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DB	3613	TACCACTGAGTGTGAGGGGTGCTCAAGGTGAAGGGCAAGGGGAGATGACCACTAC	3672
QY	3481	TTCTCTCAATGGGGGGCCAGCAGTAAACAGGGCCAGC--CACAAATTCAGCTGAAAGGA	3538
DB	3673	TTCTCTCAATGGGGGGCCAGCAGTAAACAGGGCCAGC--CACAAATTCAGCTGAAAGGA	3732
QY	3539	CCAAAGTGGGCACT	3552

Qy	1099	TTCCAAGAATCTACATACAGAAGCATGACAAATGTTCAGCATCTCTGTTTGAGACATTTGAG	1158
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Db	1135	GGCTTTCACCGCCTGGCCTCCCATGTCACATGCGCAGGAACTGTGTCATGACCTTGAATGAG	1194
Qy	1219	CTCTTTGCCCGGTTTGACAAAGCTGGCTGCGGAGAAATCACTGCTCTGAGGATCAAGATCTTG	1278
Db	1195	CTCTTTGCCCGGTTTGACAAAGCTGGCTGCGGAGAAATCACTGCTCTGAGGATCAAGATCTTA	1254
Qy	1279	GGGAGCTGTTCATCTACTGTGTTCAGGCGTGCCTGGAGGCCCGGGCCGACCATGCCCCACTGC	1338
Db	1255	GGAGACTGTTACTACTGCTGTTCAGGCGTGCCTGGAGGCCCGGGCAGATCACGCCCACTGC	1314
Qy	1339	TGTCGTGAGATGGGGGTAGACATGATTTGAGGCCCATCTCGCTGTGTAAGTGAAGGTGACAGGT	1398
Db	1315	TGTCGTGAGATGGGCGTAGACATGATCGAAGCCCATCTCGCTGTGTGCGTAGGTAAACAGGT	1374
Qy	1399	GTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGCGTGCACCTGCGCGCTCTTTGGC	1458
Db	1375	GTGAACGTGAACATGCGTGTGGGCATCCACAGCGGACGTGTGCATTTGCGGCGCTCTTGGC	1434
Qy	1459	TTGCGGAAATGGCAGTTTCGATGTGTGTCGATGATGTGACCTCTGGCCAAACCACTGAGG	1518
Db	1435	CTACGGAAATGGCAGTTTGTGTCGCTCAAAACGATGTGACCTCTGGCTAACCCACTGGAG	1494
Qy	1519	GCAGGAGCGCGGCTGCGCGCATCCATCACTTCGGCCAACTGTCAGTACTCTGAACGGG	1578
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Qy	1579	GACTACAGGTGGAGCAGCGGCGGTGTGGCGAGCGCAACGCTACTCTCAAGGAGCAGCAC	1638
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Db	1735	GACCGTGCCTTCTCCCGGACCAAGGACTCTAAGGCATTCGCCAGATGGGCATTTGATGAT	1794
Qy	1819	TCCAGCAAAGACAAACCGGGGCAACCAAGATGCCCTCGAACCTCGAGGATGAGGTGGATGAG	1878
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Qy	1939	CGGTTTCTGCTCACTTTCAGAGAGAGGATCTTGAGAAGAGTACTCCCGGAAGGTGGAT	1998
Db	1915	CGGTTCTGTCTCACTTTCAGAGAGAGGATCTTGAGAAGAGTATTCACCGGAAGTAGAT	1974
Qy	1999	CCCCGCTTCGGAGCCTACGTTTGCCTGTGCCCTGTGTGTCTTCTGCTTCATCTGCTTCATC	2058
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Qy	2059	CAGCTTCTCATCTTTCCCACTCCACCCTGANTGTGCGATCTAATGCGCATCTTCTCTG	2118
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Qy	2119	CTGCTGTCTATCACCGGTCTGATCTGTGTGTCATCTCTGTGGTTCTCTGTGTTCCCTAAG	2178
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[illegible]

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3319 TCGGGGAACACAGTGAATGTCTTAGTCGTATGGACAGCAGCGGGGTCCCCGACCGAATC 3378
Db
3295 TGGGGAATACCGTGAATGTTTCCAGTCGTATGGACAGCAGTGGAGTTCTTGACCGAATA 3354
Qy 3379 CAGGTGACCAACCGACCTGTACAGGTTCTAGCTGCCAAGGGGTACAGCTGGAGTGCGA 3438
Db 3355 CAGGTGACTACCGACCTATACCAAGTTCTAGCTGCCAAGGGGTACAGCTGGAGTGCGT 3414
Qy 3439 GGGGTGGTCAAGGTGAAGGGCAAGGGGAGATGACCCACTTCTCTCAA 3488
Db 3415 GGGGTGGTCAAGGTGAAGGGAAAGGGGAGATGACCCACTTCTCTCAA 3464

Search completed: January 7, 2004, 05:40:50
Job time : 12743 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2004, 01:25:55 ; Search time 7020 Seconds
(without alignments)
12297.649 Million cell updates/sec

Title: US-09-750-240-10
Perfect score: 3552
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_est3:*
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- 24: em_ges_pro:*
- 25: em_ges_rod:*
- 26: em_ges_phg:*
- 27: em_ges_vrl:*
- 28: gb_ges1:*
- 29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	820	23.1	1039	12	BM811640 AGENCOURT
2	812	22.9	895	14	CA487177 AGENCOURT
3	786.6	22.1	1016	13	BQ881496 AGENCOURT
4	747.4	21.0	872	14	CA453976 AGENCOURT

5	726.8	20.5	775	10	BF792125	BF792125 602252571
6	723	20.4	986	13	BUI161782	BUI161782 AGENCOURT
7	660.4	18.6	710	2	HSM071986	Bx481818 Homo sapi
8	657.8	18.5	834	13	BX355179	BX355179 BX355179
9	621.2	17.5	757	14	CA511319	CA511319 UI-R-EJ0-
10	613.8	17.3	878	14	CA487529	CA487529 AGENCOURT
11	607.8	17.1	676	10	BE840188	BE840188 QVO-FN018
12	601	16.9	740	13	BUE11374	BUE11374 UI-M-FIO-
13	593.4	16.4	711	14	CB247656	CB247656 UI-M-FIO-
14	588.4	16.3	1225	12	BI691747	BI691747 603307455
15	570.6	16.1	1043	10	BG297229	BG297229 602394937
16	569.4	16.0	743	12	BI685206	BI685206 603310213
17	568	16.0	889	13	BX451612	BX451612 BX451612
18	551.4	15.5	581	12	BG993320	BG993320 MR3-HT099
19	551.2	15.5	796	10	BG287169	BG287169 602381888
20	542	15.3	790	12	BI255147	BI255147 602977410
21	537	15.1	537	2	HSM05228	Bx501511 Homo sapi
22	532.4	15.0	890	13	BUI187098	BUI187098 AGENCOURT
23	525.2	14.8	894	14	CA488920	CA488920 AGENCOURT
24	517.6	14.6	819	13	BUI11903	BUI11903 603126114
25	512.4	14.4	905	13	BQ231940	BQ231940 AGENCOURT
26	510.8	14.4	3340	11	CNSUT117U	BX248285 human ful
27	498	14.0	607	12	BM943080	BM943080 UI-M-CGOp
28	487	13.7	487	9	ALI13686	ALI13686 DKFZp761N
29	485.8	13.7	565	12	BG872335	BG872335 602792616
30	477.6	13.4	501	13	BX474447	BX474447 DKFZp6860
31	474.8	13.4	652	9	AA207907	AA207907 mv84h06.r
32	464.8	13.1	525	12	BM090325	BM090325 505523 MA
33	459.2	12.9	737	10	BE377119	BE377119 601223107
34	456	12.8	899	13	BX420266	BX420266 BX420266
35	451.2	12.7	685	12	BM964004	BM964004 UI-M-EQO-
36	442.6	12.5	809	9	AUI169950	AUI169950 AUI169950
37	437.8	12.3	682	13	BQ180663	BQ180663 UI-M-EXO-
38	410	11.5	410	14	CA389111	CA389111 cs05f09.Y
39	407.4	11.5	420	10	BF935972	BF935972 IL2-NT019
40	405.6	11.4	453	10	BE838164	BE838164 CMI-FN010
41	405	11.4	691	14	CD217903	CD217903 pgrln.pk0
42	402.8	11.3	442	9	AI905602	AI905602 CMI-BT094-
43	402.8	11.3	466	9	AI905641	AI905641 CM-BT094-
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ALIGNMENTS

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5', mRNA sequence.
ACCESSION BM811640
VERSION BM811640.1 GI:19128463
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1039)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12712 row: 1 column: 10
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Db 1001 GTT 1003

RESULT 4
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VERSION CA453976.1 GI:24903260
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM14275 row: d column: 17
High quality sequence stop: 636.
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/lab_host="EMDH10B"
/clone_lib="NAPCL"
/notes="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dr. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,

FEATURES
source

BASE COUNT 153 a 271 c 228 g 220 t
ORIGIN
Query Match 21.0%; Score 747.4; DB 14; Length 872;
Best Local Similarity 99.9%; Pred. No. 5e-150;
Matches 748; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 GCCATGCTGGCCAAAGCTGACGGGACTCGGGCCAACTCCATGGAAGGGCTGATGCCCGC 60
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Db 121 ATTGATGATTCCAGCAAGAACAAACCGGGGACCAAGATGCCCTGAACCTTGAGGATGAG 180
Qy 1870 GTGGATGAGTTCTGAGCGGTGCGATGATGCCCGGAGCATTCATGATGAGCTGCGGAAGGAC 1929
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Db 241 CATGTGGCGGGTTCTGCTCACTTCCAGAGAGAGATCTTCAGAGAGATGACTCCCGG 300
Qy 1990 AAGGTGGATCCCGGCTTCCGAGGCTACGTTGGCTGTGCCCTGTGTGTTCTTCTGCTTCATC 2049
Db 301 AAGGTGGATCCCGGCTTCCGAGGCTACGTTGGCTGTGCCCTGTGTGTTCTTCTGCTTCATC 360
Qy 2050 TGCTTCATCCAGTCTCTCATCTTCCCACTCCACCTGATGCTGGGATCTATGCCAGC 2109
Db 361 TGCTTCATCCAGTCTCTCATCTTCCCACTCCACCTGATGCTGGGATCTATGCCAGC 420
Qy 2110 ATCTTCTGCTGCTGCTTAATCACCGTGTGATCTGCTGTGCTGCTGCTGCTGCTGCTGCTG 2169
Db 421 ATCTTCTGCTGCTGCTTAATCACCGTGTGATCTGCTGTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 2170 TTCCCTTAAGGCCCTGCAAGCTCTGTGCCCGCAGCATTTGTCCGCTCACGGGCACATAGCACC 2229
Db 481 TTCCCTTAAGGCCCTGCAAGCTCTGTGCCCGCAGCATTTGTCCGCTCACGGGCACATAGCACC 540
Qy 2230 GCAGTTGGGATCTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2289
Db 541 GCAGTTGGGATCTTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 2290 TGTAAACACACACCCCATACGAGCTGTGAGCCCGGATGCTGAATTTAACACCTGCTGAC 2349
Db 601 TGTAAACACACACCCCATACGAGCTGTGAGCCCGGATGCTGAATTTAACACCTGCTGAC 660
Qy 2350 ATCACTGCTGCCACCTGACGAGCTCAATTAATCTCTGCGGCTGGATGCTGCCCTGTGT 2409
Db 661 ATCACTGCTGCCACCTGACGAGCTCAATTAATCTCTGCGGCTGGATGCTGCCCTGTGT 720
Qy 2410 GAGGACCATGCCCCACCTGAGCTTTTC 2438
Db 721 GAGGACCATGCCCCACCTGAGCTTTTC 749

RESULT 5
BF792125
LOCUS 60252571F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4345144 5',
DEFINITION mRNA sequence.
ACCESSION BF792125
VERSION BF792125.1 GI:12097179
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM964 row: m column: 17
High quality sequence stop: 711.

Location/Qualifiers
1. .775

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:434514"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 84"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site 1:
NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT_
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC library."

BASE COUNT 184 a 199 c 239 g 153 t

Query Match 20.5%; Score 726.8; DB 10; Length 775;
Best Local Similarity 98.8%; Pred. No. 1.3e-145;
Matches 743; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 2746 GTGAGTGCAGTCCCGCTAGACTTCTCTGAAACTACAGGCAACAGGGGAGAGAG 2805

DB 11 GTGGAGTGCAGTCCCGCTAGACTTCTCTGAAACTACAGGCAACAGGGGAGAGAG 70

QY 2806 GAGATGGAGGAGCTACAGCATACAAACCGAGGCTGTGCATAACATCTGCCCAAGGAC 2865

DB 71 GAGATGGAGGAGCTACAGCATACAAACCGAGGCTGTGCATAACATCTGCCCAAGGAC 130

QY 2866 GTGGCGGCCACTTCTGGCCGGAGCGCCGATGATGAATCTACTATCAGTCGTGT 2925

DB 131 GTGGCGGCCACTTCTGGCCGGAGCGCCGATGATGAATCTACTATCAGTCGTGT 190

QY 2926 GAGTGTGTGGCTTATGTTTGCCCTCCATTGCAACTTCTGTAGTTCATGTGGAGCTG 2985

DB 191 GAGTGTGTGGCTTATGTTTGCCCTCCATTGCAACTTCTGTAGTTCATGTGGAGCTG 250

QY 2986 GAGGCAAAACAATAGGGTGTGAGTGTCTGGGCTGTCTCAACGAGATCATCGTGACTTT 3045

DB 251 GAGGCAAAACAATAGGGTGTGAGTGTCTGGGCTGTCTCAACGAGATCATCGTGACTTT 310

QY 3046 GATGAGATTATCAGGAGAGGGTTCGGGAGCTGGAAAGATCAAGCAATGTGGTAGC 3105

DB 311 GATGAGATTATCAGGAGAGGGTTCGGGAGCTGGAAAGATCAAGCAATGTGGTAGC 370

QY 3106 ACCTACATGGCTCTCAGGGCTGAACCCAGCACCTACGATCAGGTGGCGGCTCCAC 3165

DB 371 ACCTACATGGCTCTCAGGGCTGAACCCAGCACCTACGATCAGGTGGCGGCTCCAC 430

QY 3166 ATCACTGCCCTGGCTGACTACGCCATATGGGCTCATGGAGCAGATGAAGCAATCAATGAG 3225

DB 431 ATCACTGCCCTGGCTGACTACGCCATATGGGCTCATGGAGCAGATGAAGCAATCAATGAG 490

QY 3226 CACTCTTCAACAATTTTCAGATGAAGATTGGGCTGAACATGGGCCCAAGTCGTGGCAGGT 3285

DB 491 CACTCTTCAACAATTTTCAGATGAAGATTGGGCTGAACATGGGCCCAAGTCGTGGCAGGT 550

QY 3286 GTCATCGGGGCTCGAAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGT 3345
DB 551 GTCATCGGGGCTCGAAGCCACAGTATGACATCTGGGGGAACACAGTGAATGTCTCTAGT 610
QY 3346 CGTATGACAGCAGCGGGGTCCCGACCGAATCCAGTGCAGGACCTGTACCAAGTT 3405
DB 611 CGTATGACAGCAGCGGGGTCCCGACCGAATCCAGTGCAGGACCTGTACCAAGTT 670
QY 3406 CTAGTCCCAAGGCTACCAAGTGCAGGAGTGCAGGGGTGTCAGGTCGAAGGGCAAGGG 3465
DB 671 CTAGTCCCAAGGCTACCAAGTGCAGGAGTGCAGGGGTGTCAGGTCGAAGGGCAAGGG 730
QY 3466 GAGATGCACCACTACTTCTCAATGGGGGCC 3497
DB 731 GAGATGCACCACTAA--TTCTCAATGGGGGCC 760

RESULT 6

LOCUS BUI61782 986 bp mRNA linear EST 04-SEP-2002
DEFINITION AGENCOURT 7968019 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6170500
5', mRNA sequence.

ACCESSION BUI61782.1 GI:22675692

VERSION BUI61782.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 986)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13537 row: f column: 05

High quality sequence stop: 623.

FEATURES

source

1. .986 Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6170500"

/tissue_type="retinoblastoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_67"

/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Library constructed by Life

Technologies."

BASE COUNT 206 a 292 c 246 g 242 t

ORIGIN

Query Match

Best Local Similarity 97.3%; Score 723; DB 13; Length 986;

Matches 746; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

QY 2050 TGCTTATCCAGCTTCTCATCTTCCACACTCCACCTGATGTTGGATCTATGCCAGC 2109

DB 1 TGCTTATCCAGCTTCTCATCTTCCACACTCCACCTGATGTTGGATCTATGCCAGC 60

QY 2110 ATCTTCTGTGTGCTGAATACCGTGTGATCTGTGCTGTGTAATCTCTGTGTTCTGT 2169

DB 61 ATCTTCTGTGTGCTGAATACCGTGTGATCTGTGCTGTGTAATCTCTGTGTTCTGT 120

Db 682 CTGCCACCTGCAGCAGCTCAATTACTCT 710

RESULT 8
BX355179
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BX355179 834 bp mRNA linear EST 05-MAY-2003
BX355179 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
CDNA clone CS0DD002YM08 5-PRIME, mRNA sequence.
BX355179
EST.
BX355179.1 GI:30377950
Homo sapiens (human)
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 834)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6892.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DD002BG040P1&cluster=6892.f. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DD002BG04QPI.
Location/Qualifiers
1..834
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD002YM08"
/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 161 a 207 c 254 g 147 t 65 others
ORIGIN

Query Match 18.5%; Score 657.8; DB 13; Length 834;
Best Local Similarity 86.8%; Pred. No. 9.1e-131;
Matches 697; Conservative 64; Mismatches 37; Indels 5; Gaps 5;

QY 1165 ACCAGCTGGCATCCAGTGCACTGGCAGGAGCTGGTCTATGACCTGAATGAGCTCTTT 1224
DB 34 AGCAGCTGTATCCGGTCCGGAAATTCCTGGGATCTGGTATGACCTGATGAGCTCTTT 93

QY 1225 GCCCGTTTGACAAGCTGGCTCGGAGATCACTGCCTGAGGATCAAGATCTTGGGGAC 1284
DB 94 GCCCGTTTGACAAGCTGGCTCGGAGATCACTGCCTGAGGATCAAGATCTTGGGGAC 153

QY 1285 TGTACTACTGTGTCTAGGCTGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1344
DB 154 TGTACTACTGTGTCTAGGCTGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 213

QY 1345 GAGATGGGGGTAGACATGATGAGGCGCATCTCGCTGTGATGAGTGCAGCTGTGAAT 1404
DB 214 GGGATGGGGGTAGACATGATGAGGCGCATCTCGCTGTGATGAGTGCAGCTGTGAAT 273

QY 1405 GTGAACATGCGGCTGGGACATCCACAGC-GGGGCGGTGCACTCGGCGCTCTTGGCTTGG 1463
DB 274 KTKAACATGCGGCTGGGACATCCACAGC-GGGGCGGTGCACTCGGCGCTCTTGGCTTGG 333

QY 1464 GAAATGGCGATGCTGATGTGTGTCATGATGACCTTGGCGCAACCATGAGGACGAG 1523
DB 334 GAAATGGCGATGCTGATGTGTGTCATGATGACCTTGGCGCAACCATGAGGACGAG 393

QY 1524 A-GGCCGGCTGGCGCATCCATCATCTCGGGCAACACTCGAGTACCTGAACGGGGACT 1582
DB 394 RGGGGGGCTGGCGCATCCATCATCTCGGGCAACACTCGAGTACCTGAACGGGGACT 453

QY 1583 ACAGAGTGGAGCCAGCGCTGGTGGCGAGCGCAACCGCTACTCTAAGAGCAGACATTG 1642
DB 454 ACAGAGTGGAGCCAGCGCTGGTGGCGAGCGCAACCGCTACTCTAAGAGCAGACATTG 513

QY 1643 AGACTTTCTCATCTCGGGCGCCAGCCAGAAACGAAAGAGAGAGAGCCATCTGGGCCA 1702
DB 514 AGACTTTCTCATCTCGGGCGCCAGCCAGAAACGAAAGAGAGAGAGCCATCTGGGCCA 572

QY 1703 AGCTGCAGCGGACTCGGGCCCAACTCCATGGAAGGCTGATCGCGCTGGGTTCCTGATC 1762
DB 573 ARCTKACGCGGACTCGGGCCCAACTCCAWGAARGCTGATCGCGCTGGGTTCCTGATC 632

QY 1763 GTGCTTCTCCGAGCAGGACTCCAAAGGCTTCCCGCAGATGGGCAATGATGATTCGA 1822
DB 633 GTGCTTCTCCGAGCAGGACTCCAAAGGCTTCCCGCAGATGGGCAATGATGATTCGA 692

QY 1823 GCAAAGCAACCGGGGACCCCAAGATGCCCTGAACCTGAGGATGAGGTGGATGATTC 1882
DB 693 GMAAARACAAACGGGGGCMCC-AGATGCCCTGAACCTGAGGATGAGGTGGATGATTC 751

QY 1883 TGAGCGGTGCCATCGATGCCCGCAGCATTTGATGATGATGATGATGATGATGATG 1941
DB 752 TGAGCGGTGCCATCGATGCCCGCAGCATTTGATGATGATGATGATGATGATGATG 811

QY 1942 TTTCTGCTCACTTCCAGAGAGA 1964
DB 812 TTTCTGCTCACTTCCAGAGAGA 834

RESULT 9
CAS11319
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CAS11319 757 bp mRNA linear EST 15-NOV-2002
UI-R-FJ0-cpw-m-04-0-UI-r1 UI-R-FJ0 Rattus norvegicus CDNA clone
UI-R-FJ0-cpw-m-04-0-UI 5', mRNA sequence.
CAS11319
CAS11319.1 GI:25002273
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 757)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bent-soares@uiowa.edu
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 REVERSE.
Location/Qualifiers
1..757
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"

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/db_xref="taxon:10116"
/clone="UI-R-FJ0-cpw-m-04-0-UI"
/tissue_type="embryo"
/dev_stage="embryo"
/lab_host="DHI08 (Life Technologies) (T1 phage resistant)"
/notes="Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I;
UI-R-FJ0 is a cDNA library containing the following
tissue(s): rat embryo. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pY73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (drl)18 tail. The
sequence tag for this library is CATCTCTACT. This library
was created for the University of Iowa Program for Rat
Gene Discovery and Mapping (Val Sheffield, Bento Soares
and Tom Casavant)"
BASE COUNT      182 a   201 c   229 g   145 t
ORIGIN
Query Match      17.5%; Score 621.2; DB 14; Length 757;
Best Local Similarity 89.6%; Pred. No. 6.6e-123;
Matches 679; Conservative 0; Mismatches 78; Indels 1; Gaps 1;
QY 2746 GTGAGTGCAGTCCCGCTAGACTTCTCTGGAACCTACAGCAACAGGGGAGAGGAG 2805
DB 1 GTGGAATCTACCGCCCGCTGGACTTCTCTGGAACCTGCGAGGCCACAGGGAGAGGAG 60
QY 2806 GAGATGAGGAGCTACAGGCATACACCGGAGGCTGCTGATACATCTTCTGCCACAGGAC 2865
DB 61 GAGATGAGGAGTTCAGAGGCTTACACCGGCGGCTGCTGATACATCTTCTCCCAAGGAC 120
QY 2866 GTGCGCGCCACTTCTTGGCCCGGAGCGCGCAATGATGAACCTCTACTCATGTCGTGT 2925
DB 121 GTGCTGCCACTTCTTGGCCCGGAGCGCGCAACGACGAGCTGTACTACCAATCTGTC 180
QY 2926 GAGTGTGTGCTGTATGTTTGGCTTCATTCGCAACCTTCTCTGAGTTCTATGTGGAGCTG 2985
DB 181 GAGTGTGCTGTGTATGTTTGGCTTCATTCGCAACCTTCTCTGAGTTCTATGTGGAACTG 240
QY 2986 GAGCAACATGAGGCTGTGAGTGTCTGCGGTCTGCTCAACGAGATCATCGTGCATTT 3045
DB 241 GAGCGAACAATGAGGCGGTGAGTGTCTGCGACTGCTCAATGAGATCATCGCGGACTTT 300
QY 3046 GATGAGATTCATCAGCAGGAGCGGTTCCGGCAGCTGGAAGAAGATCAAGACGATTGGTAGC 3105
DB 301 GATGAGATTCATCAGTGAAGAGAGGTTCCGGCAGCTGGAAGAATCAAGACCATCGTAGC 360
QY 3106 ACTATATGCTGCTCAGGGCTGAACCGCAGCACTTACGATCAGTGTGGCGCGCTCCAC 3165
DB 361 ACTTATATGCGCGCTCCGGCTAAATGCCAGCACCTTATGACCAGGTTCGGCGCGCTGCAC 420
QY 3166 ATCACTCGCTGCTGACTAGCCATCGGCTCATGAGCAGATGAAGACATCAATGAG 3225
DB 421 ATCACTCGCTGCTGACTAGCCATCGGCTTATGAGCAATGAAGACATCAACGAA 480
QY 3226 CACTCTTCAACAAATTCAGATGAAGATTGGGCTGAACATGGGCCCGCAGTCGTCAGGT 3285
DB 481 CACTCTTCAACAAATTCAGATGAAGATCGGTTGAACATGGTCCGGTTGTAGCAGGT 540
QY 3286 GTCATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAAACACAGTGAATGTCTTAGT 3345
DB 541 GTCATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAAACACAGTGAATGTCTTAGC 600
QY 3346 CGTATGACAGCAGCGGGTCCCGACCGAATCAGGTGACCGACCGAGCTGTACCGAGTT 3405
DB 601 CGTATGACAGCAGCGAGTTCCTGACCGAATCAGGTGACCGAGCTGTCTTACCAGTT 660
QY 3406 CTAGCTGCCAAGGGCTACCAAGCTGGAGTGTGCGGGGTGGTCAAGGTGAAGGGCAAGGG 3465

|||||
661 CTAGCTGCCAAGGGCTACCAAGCTGGAGTGTGCGGGGTGGTCAAGGTGAAGGGAAAGGG 720
QY 3466 GAGATGACCACTACTTCTCTCAATGGGGCCCGCCAGCAG 3503
DB 721 GAGATGA-CACCTACTTCTCTCAATGGGGCCCGCCAGCAG 757

RESULT 10
LOCUS CA487529 878 bp mRNA linear EST 14-NOV-2002
DEFINITION AGENCOURT_10808594 MAPcL Homo sapiens cDNA clone IMAGE:6719019 5',
mRNA sequence.
ACCESSION CA487529
VERSION CA487529.1 GI:24947128
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 878)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14276 row: e column: 03
High quality sequence stop: 484.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6719019"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1
, LNCaP"
/lab_host="EMDHI08"
/clone_lib="MAPcL"
/notes="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."
BASE COUNT 201 a 234 c 273 g 170 t
ORIGIN

Query Match 17.3%; Score 613.8; DB 14; Length 878;
Best Local Similarity 98.5%; Pred. No. 2.6e-121;
Matches 641; Conservative 0; Mismatches 7; Indels 3; Gaps 2;
QY 828 GCAACTTAACCGTGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTGT 887
DB 1 GCAACTTAACCGTGTGATGCCCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTGT 60
QY 888 CTTCTGCAACAGCTCATTTGGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGGCCA 947
DB 61 CTTCTGCAACAGCTCATTTGGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGGCCA 120
QY 948 GGCCTTTTCAGGAGACCCCGGGTTTACATCCAGGCCCGGCTCCACCTCAGCATCAGAAATCG 1007
DB 121 GGCCTTTTCAGGAGACCCCGGGTTTACATCCAGGCCCGGCTCCACCTCAGCATCAGAAATCG 180
QY 1008 GCAGCAGGAGCGGCTGCTGCTGTGCGTATTGGCCCCAGCAGCTTGGCCATGGAGATGAAGA 1067
```

Db 181 GCAGCAGGAGCGCTGCTGTCGCTATGTCCTCCAGCAGCTGTCCTATGAGATGAAGA 240
QY 1068 AGACATCAACACAAAAAGAGACATGATGTTTCCACAGATCTACATACAGAGCATGA 1127
Db 241 AGACATCAACACAAAAAGAGACATGATGTTTCCACAGATCTACATACAGAGCATGA 300
QY 1128 CAATGTCAGATCCTGTTTTCAGACATGAGGCTTCCACAGCTGGCATCCAGTGCAC 1187
Db 301 CAATGTCAGATCCTGTTTTCAGACATGAGGCTTCCACAGCTGGCATCCAGTGCAC 360
QY 1188 TCGCAGGAGCTGTCATACCTGATGATGCTTTGCGCGGTTTGACAGCTGGCTGC 1247
Db 361 TCGCAGGAGCTGTCATACCTGATGATGCTTTGCGCGGTTTGACAGCTGGCTGC 420
QY 1248 GGAGATCACTGCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGAGGGCT 1307
Db 421 GGAGATCACTGCTGAGGATCAAGATCTTGGGGGACTGTTACTACTGTGTGAGGGCT 480
QY 1308 GCCGAGGCGCGGCGGCGGACCATGCTGCTGTGTGGAGATGGGGGTAGACATGATGA 1367
Db 481 GCCGAGGCGCGGCGGCGGACCATGCTGCTGTGTGGAGATGGGGGTAGACATGATGA 540
QY 1368 GCCCATCTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1427
Db 541 GCCCATCTGCTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 600
QY 1428 CA-GGGGCGGCTGCACTCGCGGCTGCTTGG--CTTGGCGAAATGSCAGTT 1475
Db 601 CAGGCGGCGGCTGCACTCGCGGCTGCTTGGCGGAAATGSCAGTT 651

RESULT 11
LOCUS BE840188 676 bp mRNA linear EST 22-SEP-2000
DEFINITION QV0-FN0181-100800-335-d08 FN0181 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE840188
VERSION BE840188.1 GI:10272566
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=4t2=qv0-FN0181-100
800-335-d08&t3=2000-08-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 625.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="FN0181"
/note="Organ: prostate normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT 125 a 203 c 193 g 155 t
ORIGIN
Query Match 17.1%; Score 607.8; DB 10; Length 676;
Best Local Similarity 97.3%; Pred. No. 4.9e-120;
Matches 618; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1585 GAGGTGAGCAGGCGGCTGGTGGCGAGCGCAACGCGTACCTCAAGGAGCAGCACATTGAG 1644
Db 2 GACCAGCAGGCGTGGCGTGGTGGCGAGCTGCAAGCGTACCTCAAGGAGCAGCACATTGAG 61
QY 1645 ACTTTCCTCATCTCGGGCGCCAGCAGCAAAACGGAAGAGAGAGCCATGCTGCCAAG 1704
Db 62 ACTTTCCTCATCTCGGGCGCCAGCAGCAAAACGGAAGAGAGAGCCATGCTGCCAAG 121
QY 1705 CTGCAGCGGACTCGGGCCCAACTCCATGCAAGGGCTGATGCCGCTGGGTTCTCTGATCGT 1764
Db 122 CTGCAGCGGACTCGGGCCCAACTCCATGCAAGGGCTGATGCCGCTGGGTTCTCTGATCGT 181
QY 1765 GCCTTCTCCCGGACCAAGGACTCCAAAGGCTTCCGCCAGATGGGCATTTGATGATTCAGC 1824
Db 182 GCCTTCTCCCGGACCAAGGACTCCAAAGGCTTCCGCCAGATGGGCATTTGATGATTCAGC 241
QY 1825 AAAGACAACCGGGGACCCCAAGATGCCCTGAACTGAGGATGAGGTGATGAGTTCCTG 1884
Db 242 AAAGACAACCGGGGACCCCAAGATGCCCTGAACTGAGGATGAGGTGATGAGTTCCTG 301
QY 1885 AGCGTGCCATCGATGCCCGCAGCATTCATCAGCTGCGGAAGAGCACATGTGCGCGGTTT 1944
Db 302 AGCGTGCCATCGATGCCCGCAGCATTCATCAGCTGCGGAAGAGCACATGTGCGCGGTTT 361
QY 1945 CTGCTCACCTTCCAGAGAGAGGATCTTCAGAGAAGTACTCCCGGAAGGTGGATCCCGCG 2004
Db 362 CTGCTCACCTTCCAGAGAGAGGATCTTCAGAGAAGTACTCCCGGAAGGTGGATCCCGCG 421
QY 2005 TTGCGAGCTACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2064
Db 422 TTGCGAGCTACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 481
QY 2065 CTGCTTCCCGCAGCTCCACCTGATGCTGGGATCTATGCGAGCATCTCTGCTGCTGCTG 2124
Db 482 CTGCTTCCCGCAGCTCCACCTGATGCTGGGATCTATGCGAGCATCTCTGCTGCTGCTG 541
QY 2125 CTAATCACCGTGTGATCTGCTGTGATCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2184
Db 542 CTAATCACCGTGTGATCTGCTGTGATCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 601
QY 2185 CAAGCTGTGCTCGCAGCATTTGCGCTCAGCGGC 2219
Db 602 CAAGCTGTGCTCGCAGCATTTGCGCTCAGCGGC 636
RESULT 12
LOCUS BU611374
DEFINITION UI-M-FIO-cau-i-13-0-UI-r1 NIH BMAP F10 Mus musculus cDNA clone
ACCESSION BU611374
VERSION BU611374.1 GI:23277589
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 740)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

FEATURES
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 Location/Qualifiers
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 /mol_type="mRNA"
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 /db_xref="taxon:10090"
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 /tissue_type="whole brain"
 /dev_stage="embryo 12.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_F10"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCAGCAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT 157 a 218 c 201 g 164 t
 ORIGIN

Query Match 16.9%; Score 601; DB 13; Length 740;
 Best Local Similarity 89.1%; Pred. No. 1.4e-118;
 Matches 660; Conservative 0; Mismatches 80; Indels 1; Gaps 1;

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 Db 1 GGCATCTTAGCAGCGGTGCAAGTGGGGGGTCCCTGGCAGCCCAATCCACAGCCCTCG 60
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 Qy 709 GCGGGCTCTGGTGGCTGGTCTTTGTCTACATCGCTTACAGCTCTCCCATCCGC 768
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 Db 61 GCGGGCTTTGGTGGCCCGGTCTTCTGTCTACATCACCCTACACTCTTCTCCCATCGC 120
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 Qy 769 ATGCGGGCTCGGCTCTCAGCGGCTGGGCTCTCCACCTTGATGATTTGGGCTGG 828
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 Db 121 ATGCGAGCGGAGTACTCAGCGGCTGGGCTCTCTACTCTGCACTTTGATTTGGGCTGG 180
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 Qy 829 CAACTTAACGTTGGTGTGCTCTCTCGAGCAGCTCGTGCCCATGTGCTGCTGTC 888
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 Db 181 CAGCTCAACAGCAGCGACCCCTCTCTTTTGAAGCAGCTCGGTGCTAACGGTGTCTTC 240
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 Qy 889 CTCTGCAACCAAGTCATTTGGCATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAG 948
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 Db 241 CTCTGCAACCAATGCCATCGGTGTCTGCACACACTACCTCTGAGTGTCTCAGCGCCAA 300
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 Qy 949 GCCTTTTCAGGAGACCCCGGTTAATCCAGCGCGGCTCCACCTGCAAGCATGAGATCGG 1008
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 Db 301 GCCTTTTCAGGAGACCCCGGTTAATCCAGCGCGGCTGCACCTGCAAGCATGAGACCGT 360
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Qy 1009 CAGCAGGAGCGGCTGCTGCTCGGTATTGGCCCGCAGCAGCTTCCCATGGAGTGAAGAA 1068
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 Db 361 CAGCAGGAGCGGCTGCTGCTATCGGTGTGGCCCGCAGCAGCTTCCCATGGAGTGAAGAA 420
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 Db 421 GACATCAACACAAAAAAGAGACATGATGTTTCCACAAGATCTTACATCCAGAACATGAT 480
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 Qy 1309 CCGGAGGCGGGCGGCGCAGCATGCCCACTGCTGTGTGAGATGCGGGGTAGACATGATGAG 1368
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 Qy 1369 GCCATCTGCTGCTAGCTGAG 1389
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 Db 721 G-CATCTGCTGCTGCTGAG 740
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RESULT 13

LOCUS

CB247656

DEFINITION

UI-M-F10-caa-e-22-0-UI.r1 NIH_BMAP_F10 Mus musculus cDNA clone

IMAGE: 6836831 5', mRNA sequence.

ACCESSION

CB247656

VERSION

CB247656.1 GI:28369300

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 711)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

The following repetitive elements were found in this cDNA

sequence: 369-390, >GC rich#low complexity (matched complement)

530-597, >TIGER1#DN/MBR2_type

Seq primer: pYX-5.

FEATURES

Location/Qualifiers

1..711

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/mol_type="mRNA"

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/db_xref="taxon:10090"

/clone="IMAGE: 6836831"

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/dev_stage="embryo 12.5dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH_BMAP_F10"

/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;

Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCAGCAC. This library was created for the University of Iowa Brain Anatomy Project (BNAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

Query Match	16.4%	Score 583.4	DB 14	Length 711
Best Local Similarity	91.6%	Pred. No. 8,7e-115		
Matches 651	Conservative 0	Mismatches 56	Indels 4	Gaps 3

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Qy	1210	CTGAATGAGCTCTTTGCCCCGTTTGACAAGCTGGCTGCGGAGAAATCACTGCCTGAGGATC	1269
Db	61	TTGAATGAGCTCTTTGCCCCGTTTGACAAGCTGGCTGCGGAGAAATCACTGCTCTGAGGATC	120
Qy	1270	AAGATCTTGGGGAGCTGTTACTACTGTGTGTACGGCTGCCGAGGCCCGGGCCGACCAT	1329
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Qy	1330	GCCACATGCTGTGGAGATGGGGGTAGACATGATTTGAGGCCCATCTCGCTGTGTACGTGAG	1389
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Qy	1450	GTCTTTGGCTTGCAGAAATGGCAGTTGCATGTGTGGTCCAAATGATGTGACCCCTGGCCAAC	1509
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Qy	1510	CACATGAGCAGGAGGCCGGCTGGCCGCATCCACATCACTCGGCGCACACTGCAGTAC	1569
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Qy	1629	GGAGACGACATTTAGAGACTTTCTCTCATCTCTGGGCGCCAGCAGAAACGGAAAGAGAGAA	1688
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Qy	1689	GGCCATGCTGGCCAGCTGACGGGACTCGGGCCCACTCCATGG-AAGGGCTGATGCCCG	1747
Db	541	AGCCATGCTGGCCAAAGCTTACGGGACACAGGGCCCACTCCATGGNAAGGACTGATGCCCG	600
Qy	1748	GCTGGGTTCCTGATCTGTGCTTCTCCCGGACCAAGGACTCCAAAGGCTTCCCGCCAGATGG	1807
Db	601	GCTGGGTTCCTGACCGTGCCTTCTCCCGGACCAAGGACTCTAAGGCAATTCGCGCAGATGG	660
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RESULT 14
BI691747
LOCUS

BI691747 1225 bp mRNA linear EST 18-SEP-2001

DEFINITION	ACCESSION	REFERENCE
VERSION	AUTHORS	
KEYWORDS	TITLE	
SOURCE	JOURNAL	
ORGANISM	COMMENT	

FEATURES

BASE COUNT
ORIGIN

Query Mat
Best Loca
Matches

Qy 27 Db

Qy Db 27

Qy	28
Db	1

Qy	28
Db	1

Qy	29
Db	2

Qy	30
Db	3

Qy 30

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mRNA sequence.
BI691747
BI691747.1 GI:15654376
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1225)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM11872 row: n column: 14
High quality sequence start: 2
High quality sequence stop: 693.

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/dev_stage="5 months"
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/note="Organ: mammary; V
Site: 2; NotI; Cloned uni
Library constructed by L
providing samples: Jeff
351 a 322 c 370 g 18

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th 16.3%; Score 578.4; DB 12; Length 1225;
Similarity 87.8%; Pred. NO. 1.1e-113;
999; Conservative 0; Mismatches 91; Indels 6; Gaps 6;

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8 TCCGCTGGCACTGTATCTGCATGCAACAAGGTGGAAATCGACTGCCCGCCCTGGACTTCCT 67
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5 CTGGAACCTACAGGCAACAGGGAGAGAGATGGAGGAGCTACAGGATACAACCG 2834
|||||
8 GTGGAAGTTACAGGCAACAGGGAGAGAGATGGAGGAGCTACAGGATACAACCG 127

5 GAGGCTGCTGCATAACATTCTGCCCAAGGACGTGGCGGCCCACTTCTTGSCCGGAGCG 2894
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8 GAGGTTGCTGCATAACATTCTTCCCAAGGACGTGGCGGCCCACTTCTTGSCCGGAGCG 187

5 CCGCAATGATGAACCTCTACTATCAGTCGTGAGTGCTGGCTGTATG-TTTGCCCTCCA 2953
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8 CCGCAACGATGAGTGTACTACCAAGTCGTGTGAATGTGTGGCTGTCATGTTTGGCTCCA 247
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4 TTGCCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAACAATGAGGGTCTCGAGTGCC 3013
8 TCGCCAAATTTCTCGAGATTCTACGTGGAGCTCGAGGCAACAACGAGGGCTGGAGTGCC 307

4 TGCGGTGCTCAACGAGATCATCGCTGACTTTGATGAGATTATCAGCGAGAGCGGTTCC 3073
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8 TGCGGTGCTCAATGAGATCATCGCAGACTTTGACGAGATCATCAGTGAGAGAGATTCC 367

4 GGCAGCTGGAAAGATCAAGACGATTGGTAGCACCTACATGGCTGCCCTCAGGGCTGAACG 3133

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2004, 05:41:19 ; Search time 1421 Seconds

(without alignments)
8680.311 Million cell updates/sec

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Perfect score: 3552

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Scoring table:

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Searched: 2276164 seqs, 1736306516 residues

Total number of hits satisfying chosen parameters: 4552328

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	3443.2	96.9	3582	10	US-09-750-240-12
5	1763.4	49.6	1812	10	US-09-750-240-3
6	1761	49.6	4523	15	US-10-175-158-1
7	883.4	24.9	2554	12	US-10-104-047-1856
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Sequence 2131, A
Sequence 17487, A
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Sequence 848, App
Sequence 457, App
Sequence 487, App
Sequence 82, Appl

ALIGNMENTS

RESULT 1
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; Sequence 10, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE OF INVENTION: FAILURE
; FILE REFERENCE: 220002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 3552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-10

Query Match 100.0%; Score 3552; DB 10; Length 3552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-10-201-000-1
; Sequence 1, Application US/10201000
; Publication No. US20020187540A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/10/201,000
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-10-201-000-1

Query Match 99.8%; Score 3545.6; DB 14; Length 4942;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3548; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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US-09-750-240-5
; Sequence 5, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.
; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; TITLE OF INVENTION: FAILURE
; FILE REFERENCE: 22002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity 99.0%; Pred. No. 0;
Matches 3517; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
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Db 61 GAACGAATGGCGAAGAGCGTTTCGCGCGCTGCGCACTCGGGCAGGTGGCTTCTGCACG 120
QY 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCGCCCTGCGGGCCCC 180
Db 121 CCCGCTATATGAGTGCCTCCGGGATGCAGAGCCACCCAGCCGCCCTGCGGGCCCC 180
QY 181 CCTCGTGCCCTCGCAGGATGAGCCCTTCAATCGAGGGGCGGCCAGGCAAGGCGCAAG 240
Db 181 CCTCGTGCCCTCGCAGGATGAGCCCTTCAATCGAGGGGCGGCCAGGCAAGGCGCAAG 240
QY 241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCAGAGTATCCAGGTGCAACGACAGCG 300
Db 241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTCAGAGTATCCAGGTGCAACGACAGCG 300
QY 301 GCGGGACGGCTGAGTGGGCGCCGACGCGGTGCCAGAGTGGGCGATCTGCTGGGCGC 360
Db 301 GCGGGACGGCTGAGTGGGCGCCGACGCGGTGCCAGAGTGGGCGATCTGCTGGGCGC 360
QY 361 CGTCTGGTGCAGGTGTTCCAGTCCAGCAGTTCGTTTCGGGCAAGCTGGAGCGCTGTAC 420
Db 361 CGTCTGGTGCAGGTGTTCCAGTCCAGCAGTTCGTTTCGGGCAAGCTGGAGCGCTGTAC 420
QY 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCTGACGCTGTGATGGCGGTGCTGTG 480
Db 421 CAGCGGTACTTTTCCAGATGAACAGAGCAGCTGACGCTGTGATGGCGGTGCTGTG 480

QY 481 CTGCTCAGCGGTGCTGCTGCTTTCCAGCCGACCCCGCCGCTCAGCCTGCCTAT 540
DB CTGCTCAGCGGTGCTGCTGCTTTCCAGCCGACCCCGCCGCTCAGCCTGCCTAT 540
QY 541 GTGGCAGTGTGGGCTGTGGGCGGCGCTGTGTGGGGCTCATGTGGTGTGTAAACGG 600
DB 541 GTGGCAGTGTGGGCTGTGGGCGGCGCTGTGTGGGGCTCATGTGGTGTGTAAACGG 600
QY 601 CATAGCTTCGCGCAGGACTCCATGTGGTGTGTAGTTACGTGGTGTGGGCTCCTGGCG 660
DB 601 CATAGCTTCGCGCAGGACTCCATGTGGTGTGTAGTTACGTGGTGTGGGCTCCTGGCG 660
QY 661 GCAGTGCAGGTGGGGGCGCTCTCGCAGCAGACCCCGCGCAGCCCTCTGGGGGCTCTGG 720
DB 661 GCAGTGCAGGTGGGGGCGCTCTCGCAGCAGACCCCGCGCAGCCCTCTGGGGGCTCTGG 720
QY 721 TGGCCTGTGTTTGTCTATACGCTTACAGCTTCCCTCCATTCGCGATTCGCGGTGCG 780
DB 721 TGGCCTGTGTTTGTCTATACGCTTACAGCTTCCCTCCATTCGCGATTCGCGGTGCG 780
QY 781 GTCTCAGCGGCTGGGCGCTCTCCACCTTGCAATTTGATCTTGGCTGGCAACTTAACCGT 840
DB 781 GTCTCAGCGGCTGGGCGCTCTCCACCTTGCAATTTGATCTTGGCTGGCAACTTAACCGT 840
QY 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCTCTGCAACCAAC 900
DB 841 GGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAATGTGCTGTCTTCTCTGCAACCAAC 900
QY 901 GTCAATTGGATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
DB 901 GTCAATTGGATCTGCACACACTATCCAGCAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
QY 961 ACCCGGTTTACATCCAGGCGCGCTCCACCTGCAGCATCAGATCGGCAGAGGCGG 1020
DB 961 ACCCGGTTTACATCCAGGCGCGCTCCACCTGCAGCATCAGATCGGCAGAGGCGG 1020
QY 1021 CTGCTGTGTCGTTATTTGCCAGCAGCTGTCATGAGATGAAAGAACATCAACACA 1080
DB 1021 CTGCTGTGTCGTTATTTGCCAGCAGCTGTCATGAGATGAAAGAACATCAACACA 1080
QY 1081 AAAAAAGACATGATGTTTCCACAGATCTACATACAGAGCATGCAATGTACAGATC 1140
DB 1081 AAAAAAGACATGATGTTTCCACAGATCTACATACAGAGCATGCAATGTACAGATC 1137
QY 1141 CTGTTTGCAGACATGAGGCTTCCAGGCTGCGCATCCAGTGCATCCAGTGCATCCAGTGC 1200
DB 1141 CTGTTTGCAGACATGAGGCTTCCAGGCTGCGCATCCAGTGCATCCAGTGCATCCAGTGC 1197
QY 1201 GTCATGACCTGATGAGCTCTTTGCCCGGTTTGACAAAGCTGGCTGGAGAAATCACTGC 1260
DB 1198 GTCATGACCTGATGAGCTCTTTGCCCGGTTTGACAAAGCTGGCTGGAGAAATCACTGC 1257
QY 1261 CTGAGGATCAAGATCTTTGGGAGCTGTGTTACTATGTGTGTGAGGCTGCGAGGCGCG 1320
DB 1258 CTGAGGATCAAGATCTTTGGGAGCTGTGTTACTATGTGTGTGAGGCTGCGAGGCGCG 1317
QY 1321 GCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATGAGGCAATCTGCTG 1380
DB 1318 GCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATGAGGCAATCTGCTG 1377
QY 1381 GTACGTGAGTGCAGGTGTGAATGTGAACATGCGGTGGGCAATCCACAGCGGCGCGTG 1440
DB 1378 GTACGTGAGTGCAGGTGTGAATGTGAACATGCGGTGGGCAATCCACAGCGGCGCGTG 1437
QY 1441 CACTGGGCGCTCTTGGCTTGGGAAATGCGAGTTCGATGTGTGGTCCAAATGATGACC 1500
DB 1438 CACTGGGCGCTCTTGGCTTGGGAAATGCGAGTTCGATGTGTGGTCCAAATGATGACC 1497
QY 1501 CTGGCCAAACCATGAGGAGGAGGCGGCGCTGGCGCATCCACATCACTCGGGCAACA 1560
DB 1498 CTGGCCAAACCATGAGGAGGAGGCGGCGCTGGCGCATCCACATCACTCGGGCAACA 1557

QY 1561 CTGCAGTACTGAAACCGGGACTACAGGTGGAGCCAGGCGGTGGCGAGCGCAACGCG 1620
DB 1558 CTGCAGTACTGAAACCGGGACTACAGGTGGAGCCAGGCGGTGGCGAGCGCAACGCG 1617
QY 1621 TACCTCAAGGAGCAGCATTGAGACTTTCTCTCATCTCTGGGCGCAGCAGAAACGGAAA 1680
DB 1618 TACCTCAAGGAGCAGCATTGAGACTTTCTCTCATCTCTGGGCGCAGCAGAAACGGAAA 1677
QY 1681 GAGGAGAAGCCACTGTGGCCAAAGCTGACGCGACTCGGSCCAACTCCATGGAAGGCGTG 1740
DB 1678 GAGGAGAAGCCACTGTGGCCAAAGCTGACGCGACTCGGSCCAACTCCATGGAAGGCGTG 1737
QY 1741 ATGCCGCGCTGGGTCTCTGATCGTGGCTTCTCCCGGACCAAGGACTCCAAAGGCTTCCGC 1800
DB 1738 ATGCCGCGCTGGGTCTCTGATCGTGGCTTCTCCCGGACCAAGGACTCCAAAGGCTTCCGC 1797
QY 1801 CAGATGGGCAATTGATGATTCAGCAAAAGACAACCGGGGACCCCAAGATGCCCTGAAACCT 1860
DB 1798 CAGATGGGCAATTGATGATTCAGCAAAAGACAACCGGGGACCCCAAGATGCCCTGAAACCT 1857
QY 1861 GAGGATGAGTGGATGAGTTCCTGAGCGCTGCGCATCGATCGATCGATCGATCGATCG 1920
DB 1858 GAGGATGAGTGGATGAGTTCCTGAGCGCTGCGCATCGATCGATCGATCGATCGATCG 1917
QY 1921 CGGAAGGACCATGTGCGCGGTTTCTGCTCACCTTCCAGAGAGGATCTTGAGAGAGAG 1980
DB 1918 CGGAAGGACCATGTGCGCGGTTTCTGCTCACCTTCCAGAGAGGATCTTGAGAGAGAG 1977
QY 1981 TACTCCCGGAAAGTGGATCCCGCTTGGAGGCTACGTTGCTGCTGCTGCTGCTGCTGCT 2040
DB 1978 TACTCCCGGAAAGTGGATCCCGCTTGGAGGCTACGTTGCTGCTGCTGCTGCTGCTGCT 2037
QY 2041 TGCTTCATCTGCTTACCTCAGCTTCTCATCTCCACACTCCACCTGATGCTGCTGCTGCTGCT 2100
DB 2038 TGCTTCATCTGCTTACCTCAGCTTCTCATCTCCACACTCCACCTGATGCTGCTGCTGCTGCT 2097
QY 2101 TATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160
DB 2098 TATGCCAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2157
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DB 2158 GGTTCCTGTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2217
QY 2221 CATAGCACCGAGTGGGCTCTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
DB 2218 CATAGCACCGAGTGGGCTCTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2277
QY 2281 ATGTTTCACTGTAACACACACCCCATACCGAGCTGTGAGCGCGGATGCTGAAATTTAACA 2340
DB 2278 ATGTTTCACTGTAACACACACCCCATACCGAGCTGTGAGCGCGGATGCTGAAATTTAACA 2337
QY 2341 CTTGCTGACATCACTGCTGCGCACTGTGAGCAGCTCAATTAATCTCTCTGGGCTGGAATGCT 2400
DB 2338 CTTGCTGACATCACTGCTGCGCACTGTGAGCAGCTCAATTAATCTCTCTGGGCTGGAATGCT 2397
QY 2401 CCCCTGTGTGAGGCGACATGCCACTGCGAGTTCCTGAGTACTTCAATCGGAGACATG 2460
DB 2398 CCCCTGTGTGAGGCGACATGCCACTGCGAGTTCCTGAGTACTTCAATCGGAGACATG 2457
QY 2461 CTGCTGAGTCTCTTGGGCGAGCTGCTGCTTCTGCGACATCAGAGCATCGGGAAGTTGGCC 2520
DB 2458 CTGCTGAGTCTCTTGGGCGAGCTGCTGCTTCTGCGACATCAGAGCATCGGGAAGTTGGCC 2517
QY 2521 ATGATCTTTGCTTGGGCTCATCTATTATTTGGTGTGCTTCTGCTGGGTCCCCCAGCCACC 2580
DB 2518 ATGATCTTTGCTTGGGCTCATCTATTATTTGGTGTGCTTCTGCTGGGTCCCCCAGCCGCC 2577
QY 2581 ATCTTTGACAACTATGACCTTCTGCTTGGGCTTCCATGCTGCTTCTTCCATGAGACC 2640
DB 2578 ATCTTTGACAACTATGACCTTCTGCTTGGGCTTCCATGCTGCTTCTTCCATGAGACC 2637
QY 2641 TTTGATGGGCTGGAATCTGCTCAGCTGAGGAGGCTGGCCCTCAAATATATATGACCCCTGTG 2700

Db 2638 TTTGATGGCTGAGCTGCTCCAGCTGCAGGAGGGTGGCCCTCAAAATATATGACCCCTGTG 2697
Qy 2701 ATTCTGCTGCTGTTGGCTGCGCTGTATCTGCAATGCTCAGCAGTGGAGTGCAGTGGC 2760
Db 2698 ATTCTGCTGCTGTTGGCTGCGCTGTATCTGCAATGCTCAGCAGTGGAGTGCAGTGGC 2757
Qy 2761 CCGCTAGACTTCTCTGGAACCTACAGGCAACAGAGGAGAGAGAGAGAGAGAGCTA 2820
Db 2758 CGCCTAAACTTCTCTGGAACCTACAGGCAACAGAGGAGAGAGAGAGAGAGAGCTA 2817
Qy 2821 CAGGCAATACAGGAGGCTGCTGCATATCATCTGCCCCAAGAGAGTGGCGGCCACTTC 2880
Db 2818 CAGGCAATACAGGAGGCTGCTGCATATCATCTGCCCCAAGAGAGAGTGGCGGCCACTTC 2877
Qy 2881 CTGGCCCGGAGCGCGCAATGATGAATCTACTACTACTAGTCTGTGAGTGTGGCTGT 2940
Db 2878 CTGGCCCGGAGCGCGCAATGATGAATCTACTACTACTAGTCTGTGAGTGTGGCTGT 2937
Qy 2941 ATGTTGCTCCTCAATGCCAACTTCTGTGATTTCTATGTGGAGCTGGAGGCAACAATGAG 3000
Db 2938 ATGTTGCTCCTCAATGCCAACTTCTGTGATTTCTATGTGGAGCTGGAGGCAACAATGAG 2997
Qy 3001 GGTGTGAGTGTGCTGGCTGCTCAACGAGATCATCGCTGACTTGTATGATGAGATTATCAG 3060
Db 2998 GGTGTGAGTGTGCTGGCTGCTCAACGAGATCATCGCTGACTTGTATGATGAGATTATCAG 3057
Qy 3061 GAGGAGCGGTTCCGGCAGCTGGAAGATCAAGAGATTTGTTAGCACCTTACATGCTGCC 3120
Db 3058 GAGGAGCGGTTCCGGCAGCTGGAAGATCAAGAGATTTGTTAGCACCTTACATGCTGCC 3117
Qy 3121 TCAGGGCTGAACCCAGCACCTTACGATCAGGTGGGCGCTCCACATCACTGCCCTGGCT 3180
Db 3118 TCAGGGCTGAACCCAGCACCTTACGATCAGGTGGGCGCTCCACATCACTGCCCTGGCT 3177
Qy 3181 GACTAGCCATCGGCTCATGAGCGAGATGAAGCATCATCATGAGCATCTCTTCAACAT 3240
Db 3178 GACTAGCCATCGGCTCATGAGCGAGATGAAGCATCATCATGAGCATCTCTTCAACAT 3237
Qy 3241 TTCCAGATGAAGTTGGGCTGAACATGGCCAGCTGTCGCGCAGGTGTCTATCGGGCTCG 3300
Db 3238 TTCCAGATGAAGTTGGGCTGAACATGGCCAGCTGTCGCGCAGGTGTCTATCGGGCTCG 3297
Qy 3301 AAGCCACAGTATGACATCTGGGGGAAACACAGTGAATGTCTTAGTGTGATGACAGCAG 3360
Db 3298 AAGCCACAGTATGACATCTGGGGGAAACACAGTGAATGTCTTAGTGTGATGACAGCAG 3357
Qy 3361 GGGGTCCCGACCGAATCCAGGTGACCGGACCTGTACAGGGTCTAGCTGCCAAGGGC 3420
Db 3358 GGGGTCCCGACCGAATCCAGGTGACCGGACCTGTACAGGGTCTAGCTGCCAAGGGC 3417
Qy 3421 TACAGCTGGAGTGTGAGGGGTGTGAGGTGAAGGGCAAGGGGAGTGAACCTTAC 3480
Db 3418 TACAGCTGGAGTGTGAGGGGTGTGAGGTGAAGGGCAAGGGGAGTGAACCTTAC 3477
Qy 3481 TTCTCAATGGGGGCCCCAGCAGTGTAAACAGGGCCCCAGGCCACAAATTCAGCTGAAGGGACC 3540
Db 3478 TTCTCAATGGGGGCCCCAGCAGTGTAAACAGGGCCCCAGGCCACAAATTCAGCTGAAGGGACC 3537
Qy 3541 AAGGTGGGCACT 3552
Db 3538 AAGGTGGGCACT 3549

RESULT 4

US-09-750-240-12
; Sequence 12, Application US/09750240
; Patent No. US20020103147A1
; GENERAL INFORMATION:
; APPLICANT: Hammon, H. K.
; APPLICANT: Insel, P. A.
; APPLICANT: Ping, P.
; APPLICANT: Post, S. R.

; APPLICANT: Gao, M.
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART
; FILE REFERENCE: 22002056723
; CURRENT APPLICATION NUMBER: US/09/750,240
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/472,667
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/008,097
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: US 08/924,757
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3582
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified AC-VI
US-09-750-240-12

Query Match 96.9%; Score 3443.2; DB 10; Length 3582;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 3491; Conservative 0; Mismatches 58; Indels 3; Gaps 1;

Qy 1 ATGTCATGTTTAGTGGCTCTCTGTCCTCTAAAGTGGATGAACGGAAACAGCCTGGGT 60
Db 22 ATGTCATGTTTAGTGGCTCTCTGTCCTCTAAAGTGGATGAACGGAAACAGCCTGGGT 81
Qy 61 GAACCAATGGCAGAGAGCTTTCGGGCGCGTGGCACTCGGGAGGTGGCTTCTGCAGC 120
Db 82 GAACCAATGGCAGAGAGCTTTCGGGCGCGTGGCACTCGGGAGGTGGCTTCTGCAGC 141
Qy 121 CCCGCTATATGAGTGTCTCCGGGATCAGAGCCACAGCCACCCCTGCGGGCCCC 180
Db 142 CCCGCTATATGAGTGTCTCCGGGATCAGAGCCACAGCCACCCCTGCGGGCCCC 201
Qy 181 CCTCGTGCCTCTGACAGGATGAGCCCTTCATCCGAGGGGGCGGCCAGGCAAGGCAAG 240
Db 202 CCTCGTGCCTCTGACAGGATGAGCCCTTCATCCGAGGGGGCGGCCAGGCAAGGCAAG 261
Qy 241 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTTCAGAGGATACCGAGGTGACACGACGG 300
Db 262 GAGCTGGGGCTGCGGGCAGTGGCCCTGGGCTTTCAGAGGATACCGAGGTGACACGACGG 321
Qy 301 GCGGGACGGCTGAGGTGGCGCCGACCGCGGTGCCAGAGTGGGCGATCCTGCTGGCGC 360
Db 322 GCGGGACGGCTGAGGTGGCGCCGACCGCGGTGCCAGAGTGGGCGATCCTGCTGGCGC 381
Qy 361 CGTCTGTGTCAGGTGTTCCAGTTCGAAGCAGTTCCTGTCGGCCAACTCGAGGCGCTGTAC 420
Db 382 CGTCTGTGTCAGGTGTTCCAGTTCGAAGCAGTTCCTGTCGGCCAACTCGAGGCGCTGTAC 441
Qy 421 CAGCGTACTTCTTCAGATGAACAGAGAGCCTGACGCTGCTGATGGCGGTGCTGGTG 480
Db 442 CAGCGTACTTCTTCAGATGAACAGAGAGCCTGACGCTGCTGATGGCGGTGCTGGTG 501
Qy 481 CTGCTCAGAGGCTGCTGCTGCTTCCACCGCCAGCCCGCCCGCCCTCAGCTCCCTAT 540
Db 502 CTGCTCAGAGGCTGCTGCTGCTTTCACCGCCAGCCCGCCCGCCCTCAGCTCCCTAT 561
Qy 541 GTGGCACTGTTGGCTGTGCGCCCGCCCTGTTTCGTGGGGCTCATGGTGTGTAAACCGG 600
Db 562 GTGGCACTGTTGGCTGTGCGCCCGCCCTGTTTCGTGGGGCTCATGGTGTGTAAACCGG 621
Qy 601 CATAGCTTCCGCCAGGACTCCATGTGGGTGTGAGTTACGTGGTGTCTGGGATCTCTGGC 660
Db 622 CATAGCTTCCGCCAGGACTCCATGTGGGTGTGAGTTACGTGGTGTCTGGGATCTCTGGC 681

Db 2839 CAGGCATCAACCGAGGCTGCTGATAACATTTCTGCCAAGGAGCTGGCGCCCACTTC 2898
Qy 2881 CTGGCCCGGAGCGCGCAATCATGAATCTCTACTATCATGTCTGTGTGAGTGTGTGCTGTT 2940
Db 2899 CTGGCCCGGAGCGCGCAATCATGAATCTCTACTATCATGTCTGTGTGAGTGTGTGCTGTT 2958
Qy 2941 ATGTTTGGCTTCATTCGCCAATCTCTCTGAGTTCTATGTGGAGCTGGAGGCAAAACAATGAG 3000
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Qy 3001 GGTGTGAGTGTGCTGGGCTGCTCAACGAGATCATGCTGACTTTGATGAGATTTATCAGC 3060
Db 3019 GGTGTGAGTGTGCTGGGCTGCTCAACGAGATCATGCTGACTTTGATGAGATTTATCAGC 3078
Qy 3061 GAGGAGCGGTTCCCGGAGCTGGAAAGATCAAGAGCATTTGGTAGCACCTTACATGCTGCC 3120
Db 3079 GAGGAGCGGTTCCCGGAGCTGGAAAGATCAAGAGCATTTGGTAGCACCTTACATGCTGCC 3138
Qy 3121 TCAGGGCTGAACCGCAGCACTTACGATCAGGTGGGCGCTCCACATCATCTGCCCCCTGGCT 3180
Db 3139 TCAGGGCTGAACCGCAGCACTTACGATCAGGTGGGCGCTCCACATCATCTGCCCCCTGGCT 3198
Qy 3181 GACTAGCGCATGCGGCTCATGAGCAGATGAAGCAGCATCAATGAGCATCTCTTTCAACAAT 3240
Db 3199 GACTAGCGCATGCGGCTCATGAGCAGATGAAGCAGCATCAATGAGCATCTCTTTCAACAAT 3258
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Qy 3361 GGGTCTCCCGACCGAATCAGGTGACGAGCACTGTACCGAGTTCTAGCTGCGCAAGGGC 3420
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Qy 3421 TACCAGCTGGAGTGTGAGGGGTGTCAAGGTGAAGGGCAAGGGGAGATGACACCTAC 3480
Db 3439 TACCAGCTGGAGTGTGAGGGGTGTCAAGGTGAAGGGCAAGGGGAGATGACACCTAC 3498
Qy 3481 TTCTCAATGGGGGCCCGCAGCAGTTTAAACAGGGCCCGCAGCCACAAATTCAGCTGAAGGGACC 3540
Db 3499 TTCTCAATGGGGGCCCGCAGCAGTTTAAACAGGGCCCGCAGCCACAAATTCAGCTGAAGGGACC 3558
Qy 3541 AAGGTGGGCACT 3552
Db 3559 AAGGTGGGCACT 3570

RESULT 5

US-09-750-240-3

; Sequence 3, Application US/09750240

; Patent No. US20020103147A1

; GENERAL INFORMATION:

; APPLICANT: Hammond, H. K.

; APPLICANT: Insel, P. A.

; APPLICANT: Ping, P.

; APPLICANT: Post, S. R.

; APPLICANT: Gao, M.

; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE HEART

; TITLE OF INVENTION: FAILURE

; FILE REFERENCE: 220002056723

; CURRENT APPLICATION NUMBER: US/09/750,240

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: US 09/472,667

; PRIOR FILING DATE: 1999-12-27

; PRIOR APPLICATION NUMBER: US 09/008,097

; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: US 08/924,757

; PRIOR FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: US 60/048,933
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: US 08/708,661
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1812
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-240-3

Query Match 49.6%; Score 1763.4; DB 10; Length 1812;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

Qy 636 TTACGTGTGTGTGGGCATCTCTGGCGCAGTCCAGTCTGGGGGCGCTCTCGCAGCAGACCC 695
Db 3 TAACGTGTGTGTGGGCATCTCTGGCGCAGTCCAGTCTGGGGGCGCTCTCGCAGCAGACCC 62
Qy 696 GCGCAGCCCTCTCTGGGCGCTCTGTGCCCTGTGTCTTCTGTCTACATCGCTACACGCT 755
Db 63 GCGCAGCCCTCTCTGGGCGCTCTGTGCCCTGTGTCTTCTGTCTACATCGCTACACGCT 122
Qy 756 CCTCCCATCCGATGCGGGCTGCGGCTCTCTCAGCGGCTCTCCACCTTGCATTT 815
Db 123 CCTCCCATCCGATGCGGGCTGCGGCTCTCTCAGCGGCTCTCCACCTTGCATTT 182
Qy 816 GATCTTGGCTGGCAACTTAACCGTGTGTGATGCTTCTCTGGAAGAGCTCGGTGCCAA 875
Db 183 GATCTTGGCTGGCAACTTAACCGTGTGTGATGCTTCTCTGGAAGAGCTCGGTGCCAA 242
Qy 876 TGTGCTGCTGTTCTCTGACCAACGTCATTTGGGATCTGACACACTATCAGCAGAGGT 935
Db 243 TGTGCTGCTGTTCTCTGACCAACGTCATTTAGCATCTGCAACAACATCAGCAGAGGT 302
Qy 936 GTCTCAGCGCCAGGCTTTTCAAGAGACCGCGGTTTACATCCAGGCGCGGCTCCACCTGCA 995
Db 303 GTCTCAGCGCCAGGCTTTTCAAGAGACCGCGGTTTACATCCAGGCGCGGCTCCACCTGCA 362
Qy 996 GCATGAGATCGGCGAGGAGCGGCTGCTGCTGTGCTGATTTGCCCGAGCAGTTGCCAT 1055
Db 363 GCATGAGATCGGCGAGGAGCGGCTGCTGCTGTGCTGATTTGCCCGAGCAGTTGCCAT 422
Qy 1056 GGAGATGAAGAAGACATCAACACAAAAAAGAGACATGATGTTTCAACAAGATCTCAT 1115
Db 423 GGAGATGAAGAAGACATCAACACAAAAAAGAGAC---ATGTTTCAACAAGATCTCAT 479
Qy 1116 ACAGAAGCATGACAATGTACGATCTCTGTTTTCAGACATTTGAGGGCTTCCACGAGCTGGC 1175
Db 480 ACAGAAGCATGACAATGTACGATCTCTGTTTTCAGACATTTGAGGGCTTCCACGAGCTGGC 539
Qy 1176 ATCCAGTGCATCGCGAGGAGCTGGTCATGACCTGATGAGTCTTTTGGCCCGGTTTGA 1235
Db 540 ATCCAGTGCATCGCGAGGAGCTGGTCATGACCTGAAATGAGCTCTTTTGGCCCGGTTTGA 599
Qy 1236 CAAGCTGCTGCGGAGAACTCACTGCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTG 1295
Db 600 CAAGCTGCTGCGGAGAACTCACTGCTGAGGATCAAGATCTTTGGGGGACTGTTACTACTG 659
Qy 1296 TGTGTGAGGGCTGCGGAGGCGCGGCGGCGACCATGCCACCTGCTGTGTGGAGATGGGGGT 1355
Db 660 TGTGTGAGGGCTGCGGAGGCGCGGCGGCGACCATGCCACCTGCTGTGTGGAGATGGGGGT 719
Qy 1356 AGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTAATGTGAACATCGG 1415
Db 720 AGACATGATTGAGGCCATCTCGCTGGTACGTGAGGTGACAGGTGTAATGTGAACATCGG 779
Qy 1416 CGTGGGATCCACAGCGGCGGCTGCTGCGGGCTCTCTTGGCTTGGGAAATGSCAGTT 1475
Db 780 CGTGGGATCCACAGCGGCGGCTGCTGCGGGCTCTCTTGGCTTGGGAAATGSCAGTT 839
Qy 1476 CGATGTGTGTGTTCAATGATGTGACCTTGGCCCAACACATGAGGCGAGGCGCGGCTGG 1535

Db	3430	CGGCTACTCAATGAGATCATCGCTGACTTTGATGAGATCATCAGCAGGATCGGTTCCGG	3489
Qy	3076	CAGCTGGAAGAAGATCAAGACGATTGGTAGCACCTACATGATGCTGCTCAGGGCTGAAGCC	3135
Db	3490	CAGCTGGAAGAAGATCAAGACGATTGGTAGCACCTACATGATGCTGCTCAGGGCTCAACGAC	3549
Qy	3136	AGCACCTACGATCAGGTGGGCGCTCCACATCACTGCCCTGGCTGACTACGCCATCGG	3195
Db	3550	TCTACCTACGACCAAGGTGGGCAAGACCCACATCAAGGACTGGCCGACTTTGCCATGAAG	3609
Qy	3196	CTCATGGAGCAGATGAAGCACATCAATGAGCACTCTTCAACAAATTTCCAGATGAAGATT	3255
Db	3610	CTGATGACACAGATGAAGTACATCAATGAGCACTCTTCAACAAATTTCCAGATGAAGATC	3669
Qy	3256	GGGCTGAACATGGGCCCACTGTCGACAGGTGTCTAGTGTGATGACAGCAGCGGGTCCCGACCGA	3315
Db	3670	GGGCTCAACATCGGCCCGCTGGTGGCGGGGTGATAGGGGCAAGAAAGCCCTCAGTACGAC	3729
Qy	3316	ATCTGGGGGAACACAGTGAATGTCTCTAGTGTGATGACAGCAGCGGGGTCCCGACCGA	3375
Db	3730	ATCTGGGGCAATACCGTGAAGCTGGCCAGCGCATGACAGCACCGGTGTACCCGACCGC	3789
Qy	3376	ATCCAGGTGACACCGGACCTGTATACAGGTTCTAGCTGCCAAGGGCTACCACTGGAGTGT	3435
Db	3790	ATCCAGGTGACACCGGACCTGTATACAGGTTCTAGCTGCCAAGGGCTACCACTGGAGTGT	3849
Qy	3436	CGAGGGTGTCAAGGTGAAGGGCAAGGGGAGATGACCACTTCTCCTCAATGGGGG	3495
Db	3850	CGGGCGGTGGTCAAGGTCAAGGGCAAGGGGAGATGATGACCTTCTCCTCAATGGAGGG	3909
Qy	3496	CCC 3498	
Db	3910	CCC 3912	

RESULT 7
US-10-104-047-1856
; Sequence 1856, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1856
; LENGTH: 2554
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1856

Query Match 24.9%; Score 883.4; DB 12; Length 2554;
Best Local Similarity 71.8%; Pred. No. 5.7e-241;
Matches 1208; Conservative 0; Mismatches 451; Indels 24; Gaps 3;

Qy	855	CTGGAAGCAGCTCGGTGCGCAATGTGCTGCTTCTCTGACCAACGTCATTTGGCATCTG	914
Db	114	CAGTGAGAGCTTGTCTCCAAATGTTCTCATTTTCTCTGACCAACATCGTGGGTGCTG	173
Qy	915	CACACATATCCAGCAGAGGTGTCTCAGCGCAGGCTTTTCAGAGACCCCGGTTACAT	974
Db	174	CACCACTATTCGGCTCAGGTCCCGCAGAGACAGGCTTTCCAGGAGACCCGAGAGTGCAT	233
Qy	975	CCAGGCCGCTCCACCTCGAGCATGAGATCGGCAGCAGGCGGTCTGCTGCTGCT	1034
Db	234	CCAGCGCGGTCCACTCGCAGTGGGAGAACACAGCAGAGGAGCGGTCTGCTGCTGT	293
Qy	1035	ATTGCCCCAGCACGTTGCCATGGAGATGAAGAAGACATCAACACAAAAAAGAGACAT	1094

Db	294	CTTCCCTCCGCTCATGTTGCCATGGAGATGAAGCAGACATCAACGCCAAGCAGGAGATAT	353
Qy	1095	GATGTTCCACAGAGATCTACATACAGAAAGATGACAAATGTGACGATCTGTTTCCACACAT	1154
Db	354	GATGTTCCATAAGATTACATCCAGAAACATGACAAATGAGCATCTGTTTCCGATCAT	413
Qy	1155	TGAGGGCTTCCACAGCCTGSCATCCCAAGTGCATCGCGCAGGAGCTGTCATGACCCCTGAA	1214
Db	414	CGAGGGCTTCCACAGCCTGSCATCCCAAGTGCATCGCGCAGGAACTGTCATGACCCCTCAA	473
Qy	1215	TGAGCTCTTTTGGCCCGGTTTGACAAAGCTGGCTGCGGAGAAATCACTGCTGAGGATCAAGAT	1274
Db	474	CGAGCTCTTTCCCGCCGCTTTTGACAAAGCTGGCCGAGAGAAATCACTGTTTACGTTAAGAT	533
Qy	1275	CTTGGGGGACTGTATTACTGTGTGTGACGGCTGCCGAGGCGCCGCGCCGACCATCGCCCA	1334
Db	534	CTTGGGGGATTTGTTATTACTGTGCTCTCGGGGCTGCCGAGCAAGGGCTGACACCGCCCA	593
Qy	1335	CTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTGTGATGAGGTGAC	1394
Db	594	CTGCTGTGTGGAGATGGGGATGACATGATGAGGGCCATCTCGTTGTCGGGAGGTGAC	653
Qy	1395	AGGTGTGAATGTGAACATCGCGTGGGCTATCCACAGCGGCGGTGCATCTGCGGCGTCT	1454
Db	654	AGGGGTGAACGTGAACATCGGTGTGGAAATTCACAGCGGCGGAGTACACTGCGGTGTCT	713
Qy	1455	TGCTTGGCGAAATGCGAGTTGATGTGTGTTTCAATGATGTGACCTGCGCCAAACCAT	1514
Db	714	TGCTTCTCAGGAAGTGGCAGTTTCAGCGTCTGCTGTAAAGTGTGACGCTAGCCAAACCAT	773
Qy	1515	GGAGGCGAGAGCGCGGCTGGCGCATCCACATCACTCGGGCAACACTGCGAGTACCTGAA	1574
Db	774	GGAGGCTGGCGCAAGCGAGCGCATCCACATCCAAAGGCTTACACTCACTTACCTGAA	833
Qy	1575	CGGGGCTACGAGGTGAGCCAGGCGTGTGTGCGAGCGCAACCGCTTACTCAAGAGCA	1634
Db	834	TGGGGCTACGAGGTGAGCCAGGCTGTGGGGCGAGCGCAACCGCTTACTCAAGAGCA	893
Qy	1635	GCATTTGAGACTTTTCTCTATCTGCGCGCAGCGCAAGAAACGGAAGAGAGAGGCCAT	1694
Db	894	CAGTATCGAGACCTTCTCTATCTGCGCTGCAACCCAGAAAGCGGAAAGAGAGAGGCCAT	953
Qy	1695	GCTGGCCAAAGCTGACGCGGACTCGGGCCAACTCCATGGAAGGGCTGATGCGCGCTGGGT	1754
Db	954	GATCGCAAGATGAACTCCAGAGAACCAACTCCATCGGGCAACCCACCACTTGGGG	1013
Qy	1755	TCTGATCGTGCCTTCTCC-----CGGACCAAGGACTCCAAAGSCCTTCCGCCA	1802
Db	1014	GGCTGAGCGCCCTTCTCAAAACCCCTGGGTGGCAACAGGTGTCTCAAGGAGATGAAGCG	1073
Qy	1803	GATGGGCATTTGATGATTCAGCAAGCAACCGGGGCAACCAAGATGCTTGAACCTGA	1862
Db	1074	GATGGGCTTTTGAAGACCCCA-----AGGACAAAGAACCGCCAGAGAGTGCAGAACCTGA	1127
Qy	1863	GGATGAGGTGGATGAGTTCTGAGCGGTGTCATTCGATGCGCGCAGCATTTGATCAGCTGCG	1922
Db	1128	GGATGAGGTGGATGAGTTCTGCGCGCTGCGATTTGACCGCAGGAGCATTTGATAGGCTCG	1187
Qy	1923	GAAGGACCATGTGCGCGGTTTCTGCTCACCTTCCAGAGAGAGGATCTTTGAGAAGAAGTA	1982
Db	1188	GTCTGAGCAGCTCCGCAAGTTCTCTGCTGACCTTTCAGGGAGGCTGACTTAGAGAAGAAGTA	1247
Qy	1983	CTCCCGAAGGTGGATCCCGCTTCCGAGGCTAGTGTGCTGCTGCTGCTGCTGCTGCTG	2042
Db	1248	CTCAAGCAGGTAGACGACCGATTTTGGTGCCTATGTTGGCGTGTGCTGCTGCTGCTGCT	1307
Qy	2043	CTTCACTGCTTCTCATCTCTCATCTTCCACACTCCACCTCATGATGCTTGGGACTTA	2102
Db	1308	CTTCACTGCTTCTCATCTCTCATCTTCCACACTCCACCTCATGATGCTTGGGACTTA	1367
Qy	2103	TGCCAGCATCTTCTGCTGCTGCTAATCAACCGGTGCTGATGCTGCTGCTGCTGCTGCTG	2162

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; PRIOR FILING DATE: 2000-11-08
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
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; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14

; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
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; PRIOR FILING DATE: 2000-10-20
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; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14

Query Match 16.8%; Score 590.8; DB 11; Length 837;

Best Local Similarity 85.7%; Pred. No. 9.9e-158;

Matches 655; Conservative 1; Mismatches 108; Indels 0; Gaps 0;

Qy	2735	ATGCTCAGCAGGTGGAGTCGACTGCCCGCTAGACTTCTCTGGAACACTACAGGCAACAG	2794
Db	1	ACGCCCAGCAGGTGGAGTCACCTGCCCGCTCGACTTCTCTGGAGACTCGAGCCACAG	60
Qy	2795	GGGAGAGGAGGAGATGAGGAGCTACAGGCATACAAACCGAGGCTGCTGCATAACATTC	2854
Db	61	AGGAGATAGGAGATGAGGAGCTGACAGGCTTACAAACCGGCGGCTGTCACACATCC	120
Qy	2855	TGCCCAAGGACGTGGCGGCCACTTCTGGCCCGGAGGCGCCGCAATGATGAATCTTACT	2914
Db	121	TGCCCAAGGACGTGGCGGCTCACTTCTGGCCCGGAGGCGGCAATGATGAGCTTACT	180
Qy	2915	ATCAGTCGTGTGAGTGTGGCTGTTATGTTTGGCTTCCATTGCGCAACTCTCTGAGTTCT	2974
Db	181	ATCAGTCGTGTGAGTGTGGCGGTGATGTTCCGCTTCCATCGGCAACTCTCTCGAGTTCT	240
Qy	2975	ATGTGAGCTGGAGGCAACAAATGAGGCTGTTCAGTGCCCTGCGGCTGCTCAAGAGATCA	3034
Db	241	ACGTTGAGCTGGAGGCAACAAACGAGGCTGTTCAGTGCCCTGCGGCTTCAATGAGATCA	300
Qy	3035	TGCTGACTTTGATGAGATTATCAGCAGGAGGCGGTTCCGGAGCTGGAAAGATCAAGA	3094
Db	301	TCGCTGACTTTGATGAGATCATCAGCAGGAGTCCGTTCCGGAGCTGGAAAGATCAAGA	360
Qy	3095	CGATTGTAGCCTTACATGGCTGCTCAGGCTGGAACGCCACACCTACGATCAGTGG	3154
Db	361	CAATCGGACACCTACATGGCTGCTTCCGCTTCAAGACTTACTACGACAGGTTG	420
Qy	3155	GCGCTCCACATCCTGCTGCTGCTGACTACGCCATGCGGCTCATGGAGCAGATGAAGC	3214
Db	421	GCAAGACCCACATCAAGGCCTGGCCGACTTTGCCATGAAGCTGATGGACCATGAAGT	480
Qy	3215	ACATCAATGAGCACTCTTCAACAATTCAGATGAAGATTGGGCTGAGACATGGGCCAG	3274
Db	481	ACATCAATGAGCACTCTTCAACAATTCAGATGAAGATTGGGCTCAACATCGGCCCG	540
Qy	3275	TGCTGCGAGTGTCTATCGGCGCTCGGAAGCCACAGTATGACATCTCGGGGAAACAGTGA	3334
Db	541	TGCTGCGCGGCTGATAGGGGACAGAAAGCTTCACTACGACATCTGGGGCAATACCGTGA	600
Qy	3335	ATGCTCTTAGTCTGATGGACAGCAGCGGGGTCCCGACCGGAATCCAGGTGACCCAGACC	3394
Db	601	ACGTGGCCAGCCGATGGACAGCAGCGGTGTACCCGACCGCATCCAGGTCAACACAGACA	660
Qy	3395	TGTACAGGTTCTAGCTGCCAAGGGCTACAGCTGAGTGTTCAGGGGTGTTCAAGTGA	3454
Db	661	TGTACAGGTTCTAGCTGCCAAGGGCTACAGCTGAGTGTTCAGGGGTGTTCAAGTGA	720
Qy	3455	AGGGCAAGGGGAGATGACCACTTCTCTCAATGGGGCCCC	3498
Db	721	AGGGCAAGGGGAGATGACCACTTCTCTCAATGGAGGGCCCC	764

RESULT 9

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; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
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; PRIOR FILING DATE: 2000-10-13
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; PRIOR FILING DATE: 2000-09-06
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; PRIOR APPLICATION NUMBER: 60/241,826
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14

Query Match 14.9%; Score 528.6; DB 11; Length 915;

Best Local Similarity 85.7%; Pred. No. 5.7e-140;

Matches 599; Conservative 0; Mismatches 99; Indels 1; Gaps 1;

QY

2800 AAGGAGGATGGAGGAGCTACAGGATACACCGAGGCTGTGCATAACATTCTGCC 2859

Db 17 AAAGAGGAGATGAGAGAGCTGCA-GCCTACAAACCGCGCGCTCTCTGCACAACTCTCGCC 75
Qy 2860 AAGGACGTGGCGCCACCTTCTGCGCGGAGCGCGCAATGATGAACTCTACTATCAG 2919
Db 76 AAGGACGTGGCGCCACCTTCTGCGCGGAGCGCGCAATGATGAACTCTACTATCAG 135
Qy 2920 TCGTGTGAGTGTGGCTGTATGTTGCTCCATGTCCTCAATGTCCTCTCTGAGTTCTATGTG 2979
Db 136 TCGTGTGAGTGTGGCGGTGATGTTGGCTCCATCGCCAACTTCTCGAGTTCTACGTT 195
Qy 2980 GAGCTGGAGGCAAAACAATGAGGGTGTGAGTGCCTGCGGCTCTCAACGAGATCATCGT 3039
Db 196 GAGCTGGAGGCAAAACAAGAGGGTGTGAGTGCCTGCGGCTCTCAATGAGATCATCGT 255
Qy 3040 GACTTTGATGAGATTATCAGCAGAGCGGTTCCGCGAGCTGGAAGATCAAGACGATT 3099
Db 256 GACTTTGATGAGATCATCAGCAGAGTCTGTTCCGCGAGCTGGAAGATCAAGACCATC 315
Qy 3100 GGTAGCACCCTACATGGCTGCTCAGGGCTGAAAGCGCAGCACCCTACGATCAGGTGGCGCG 3159
Db 316 GGCAGCACCTACATGGCTGCTCAGGGCTCAGGGCTCAAGGACTCTACCTACGACAGGTGGCGAAG 375
Qy 3160 TCCACATCAGTCCCTGCTGACTACGCGCATGCGGCTCATGAGCAGATGAAAGCACATC 3219
Db 376 ACCCACATCAAGGCACTGGCGACTTGGCATGAAGCTGATGGACGAGATGAAGTACATC 435
Qy 3220 AATGAGCACTCTTCAACAATTTCCAGATGAGATGGCTGAAATGGCCACCTGCTG 3279
Db 436 AATGAGCACTCTTCAACAATTTCCAGATGAGATGGGCTCAACATCGGCCCCGTGGTG 495
Qy 3280 CGAGGTGTCATCGGGGCTCGGAAGCCACAGTATGACATCTGGGGGAAACACAGTGAATGTC 3339
Db 496 GCGCGGGTGATAGGGGCGACGAAGCTCAGTACGACATCTGGGGCAATACCTGAACTGTG 555
Qy 3340 TCTAGTGTATGAGCAGACGCGGGGTCCCGACCGAATCCAGGTGACCAAGGACCTGTAC 3399
Db 556 GCCAGCCGATGAGCAGCAGCAGCGGTGTACCCGACCGCATCCAGGTCAACACAGATGTAC 615
Qy 3400 CAGGTTCCTAGCTGCCAAGGGCTACAGCTGGAGTGTCCGAGGGGTGTCAGAGTGAAGGC 3459
Db 616 CAGGTGTGCTGCTGCCAACAACAGTACAGCTGGAGTGTCCGAGGGGTGTCAGAGTGAAGGC 675
Qy 3460 AAGGGGAGATGACCACTTCTCTCAATGGGGGCCCC 3498
Db 676 AAGGCGAGATGATGACCTTCTCTCAATGGAGGGCCC 714

RESULT 11
US-10-121-911-2
; Sequence 2, Application US/10121911
; Publication No. US20020164632A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/10/121,911
; PENDING FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/09/412,210
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: 21529 adenylate cyclase
; NAME/KEY: CDS
; LOCATION: (247)...(3480)
US-10-121-911-2

Query Match 14.4%; Score 512.4; DB 14; Length 3518;
Best Local Similarity 49.8%; Pred. No. 4.e-135;
Matches 1571; Conservative 0; Mismatches 1506; Indels 75; Gaps 8;
Qy 409 GAGCGCTGTATCCAGCGGTACTTCTTCCAGATGAACAGAGAGAGCTTCACTGCTGTATG 468
Db 286 GACTCTTCTTACGAGACCTACTACAGCCTGAGCAGCAGTACCGGCTCTGCTGTGCTG 345
Qy 469 GCGGTGTGTGTGCTCAGCAGCGGTGCTGCTGCTTCCAGCGCGCAGCCGCGCCCT 528
Db 346 CTGGGATCTGTGCTCTGTGCGCTCGCGGCTGTCTGCGAGTGGCTTGGCGCAGCGGAG 405
Qy 529 CAGCGCTGCTATG-----TGGCACTGTGTGGCTGTGCGCGCGCTGTGTCTGTG 576
Db 406 GAGCTGACTCAGACCCGAGCTTCTTACCACTGTGTGCTGTGCGGCTGGCGGCTTCTCG 465
Qy 577 GGGCTCATGTGTGTGTAAACCGGATAGCTTCCGCGAGGACTCAATGTGGTGTGAGT 636
Db 466 CTGCTGTGGGCTCGCTTCCCGGAGCAGGACTGACGCGTGGACGCTCCCTGTCC 525
Qy 637 TACGTGTGTGGGATCTCGCGCGAGTGCAGGTCCGGGGGCTCTCGCAGCAGACCG 696
Db 526 GGTGTGTGTGGTGTGGCTGTAGCGCTAGGCGACGCTTCTGTTCACCGGGGCGTG 585
Qy 697 CGCAGCCCTCTCGGGGCTCTGTGTGCTGTCTTGTCTATCATCGCTTACACGCTC 756
Db 586 GTGAGCGCTGGGACGAGTGTCTTATTTCTTCTGTCTATCTTACGCGGTATGCGATG 645
Qy 757 CTCCCGATCCGATCGCGGCTGCGCTCTCAGCGGCTGGGCTTCCACCTTGCATTG 816
Db 646 CTGCGCTTGGGATGCGGAGCGCGCTGCGGGCTCTGCTCTCTACTCTGCTATCTG 705
Qy 817 AT-----CTTGGCTGGCACTTAAACGCTGGTGTGCTTCTCTG---GAAGCAG 864
Db 706 CTGTGTCTCGGCTGTATCTTGGGCGACAGCGGACTCAGCGCTGCACTGCTGCGCGAG 765
Qy 865 CTGCGTGCATATGTGTCTCTCTGCAACCAAGCTTATGGCATCTGTCACACACTAT 924
Db 766 TTGGCAGCAACGCGTGTCTTCTGTGCGGAACTGGCAGGAGTGTACCAAGGCG 825
Qy 925 CCAGCAGAGTGTCTCAGCGCAGGCTTTTCAGAGACCCCGGTATACATCCAGGCGCG 984
Db 826 CTGATGAGCGCGCTTCCGCGGCGACCTTCCGCGGAGCACTCAGCTCTCTGCACTCAGC 885
Qy 985 CTCCACCTGAGCATGAGAATCGCAGCAGGCGGTGCTGTGCTGTGCTGATTTGCCCGAG 1044
Db 886 CGGCGGCTGGACACCGAGAGAACCAACCAACCTTCTTGTTCATCTCTCTGCTGCC 945
Qy 1045 CACGTTGCTATGGAGATGAAAGAGACATCAACACAAAAAAGAAGA----- 1091
Db 946 TACCTGGCCCGAGAGATGAGGCGAGATATGCGCGCTGCGAGGAGGAGGCTCA 1005
Qy 1092 -----CATGATGTTCCCAAGATCTACATACAGAGCATGACAAATGTCAGC 1137
Db 1006 CGGCGAGAGACACTAACAATTTCCACAGCTCTATGTCAAGAGGACACAGGAGTCA 1065
Qy 1138 ATCTGTTTGCAGACATGAGGCTTCCAGCGCTTGGCATCCAGTGCATCTGCGGAGAG 1197
Db 1066 GTGCTGTATGTGATCTGCGGCTTCAACGCGGTGCGCAGGAGTGTTCCTCCCTAAGGAG 1125
Qy 1198 CTGGTTCATGACCTGAAATGAGCTCTTTCGCCGCTTTCAGAGCTGGCTGCGGAGATCAC 1257
Db 1126 CTGGTGTCTATGCTCAATGAGCTCTTTGGCAAGTTTCGACAGATGTCAGAGAGCATGAA 1185
Qy 1258 TGCCTGAGGATCAAGATCTTGGGGGACTGTTTACTACTGTGTGTGCTGAGGCTGCCGAGGCC 1317
Db 1186 TGCATGGGATCAAGATCTCTGGGAGCTGTTTACTACTGTGTCTCTGCGGCTGCCACTCTCA 1245
Qy 1318 CGGCGGACCATGCCACTGCTGTGTGAGATGGGGGTAGACATGATTTGAGGCCATCTCG 1377
Db 1246 CTGCCAGACCATGCCATCAACTGCGGTGCGCATGGGCGCTGGACATGTGCCGGGCGCATCAGG 1305

Qy	1378	CTGGTACGTGAGGTGACAGGTGTGAATGTGAAATCATGCGCGCTGGGCATCCACACGCGGGCGC	1431
Db	1306	AAACTGCGGGCAGCACACTGGCGGTGGACATCAACATGCGTGTGGCGGTGCACTCAGGCAGC	1365
Qy	1438	GTGCACACTGCGGCGTCTTGTGCTTGCAGAAATGACAGTTCCATGTGTGGTCCAAATGATGTG	1497
Db	1366	GTACTGTGTGGAGTTCATCGGGCTGCGAAGTGGCAGTACACAGCTTTGGTCACATGATGATC	1425
Qy	1498	ACCTGGCCAAACCATATGAGGAGGAGGCGGGCTGGCCGCACTCCACATCACTCCTCGGGCA	1557
Db	1426	ACACTGGCTAAACCATGATGAGGACGAGCGGTATCCAGGGCGAGTGCACATCAAGGGGCT	1485
Qy	1558	ACACTGCAGTACTTGAAACGGGGACCTACGAGGTGAGACGAGCGCGTGTGTGGCAGCGCAAC	1617
Db	1486	ACCTGGCCCTGTGTGGCAGGGGCTTATGCTGTGGAGGACGACGAGCATGAGCATCGGGAC	1545
Qy	1618	GGGTACCTCAAGGAGCAGCACAATTGAGACTTTTCTCATCTCTGGGGCCAGCCAGAAACGG	1677
Db	1546	CCCTTACCTTCGGGAGCTAGGGGAGCCTACCTATCTTGGTCAATCGATCCACGGGCAGAGGAG	1605
Qy	1678	AAAGAGAGAGAGGCCATGCTGGCCAAAGCTGCAGCGGACTCGGGCCAACTCCATGGAAGGG	1737
Db	1606	GAGGATGAGAAAGGCACATGCAGGAGGCTTGCTGTCTCGCTTGAGGGCCTCAAGATGCGT	1665
Qy	1738	CTGATGCGCGCTGGGTCTCTGATCTGTGCTTCTCCGGACCAAGGACTCCAAAGGCGCTTC	1797
Db	1666	CCATCACTGTGATGACCCGTTACTTGGAGTCTCTGGGGGGCAGCAAGCCTTTTGGCCAC	1725
Qy	1798	CGCCAGATGGGCATTGATGATTTCCAGCAAAAGACAAACGGGGGACCCCAAGATGCCCTG--A	1855
Db	1726	CTGAGCCACCGGAGACAGCCCTGTGTCCACTCCACCCCTCTCCCGGAGAAAGACCTTGCGT	1785
Qy	1856	ACCTGAGGATGAGGTGGA-TGAGTTCTTGAGCGCTGCCATCGATGCCCGCAGCATTTGAT	1914
Db	1786	TCCTTCAGCACCCAGTGGAGCTGGATCGAGGCGGTACCCCGGGGACTAGATGATGA	1845
Qy	1915	CAGTCGGGAAGGACCAATGTGCGCGGTTTTCTGCTCACTTCCAGAGAGAGSACTTTGAG	1974
Db	1846	CTGGACACCGGGATGCCAAGTTCTTCCAGGTCAATTGAGCAGCTCAACTCGCAGAAACAG	1905
Qy	1975	AAGAGTACTCCCGGAAGGTGGATCCCGGCTTCGGAGCCTACGTTGCGCTGTGCCCTGTTC	2034
Db	1906	TGGAAGCAGTTCGAAGGACTTCAACCCCACTGCACACTGTACTTCAAGAGAAAGSAGATGGAG	1965
Qy	2035	GTCTTCGTTCATCTGCTTTCATCCAGCTTCTCATCTTCCACACTCCACCCCTGATGCTT	2094
Db	1966	AAAGATACCGACTCTCTGCAATCCCGCGCTTCAATACTATGAGCGCTGCACCTTCCTG	2025
Qy	2095	GGGATCTATGCCAGCATCTTCTGCTGCTGCTAATCAACCGTGTGATCTGTGCTGTGTAC	2154
Db	2026	GTTTTTCTCTCCAACTTCATCATCCAGATGCTAGTGACAAAGGCCCCCGAGCTCTGGCC	2085
Qy	2155	TCTGTGGTTCCTGTTCCTTAAGGCCCTTGGAAGTCTGTCCGCGACGATGTGCCGTCA	2214
Db	2086	ATCAC---GTATAGCATCACTTTCCTCCTCTCTTCCTCATCTCTTTTGTCTGCTCTCTCA	2142
Qy	2215	CGGSCACATAGCACCGCAGTTGGCATCTTTTTCGTCTGTCTGTGTGTTTACTTCTGCGCATT	2274
Db	2143	GAGGACCTGATGAGGTGTCTTGAAAGGGCCCCAAGATGTGCACTGGCTGCTGCACACTG	2202
Qy	2275	GCCAAACATGTTCACTGTAACCAACACCCCCCATAGCGAGCTGTGCAGCCCCGGATGCTGAAT	2334
Db	2203	TCTGGCCTGTGGCCACACGACCAGGACTAGAAATAGCCTTGGGCACCGCCACCATCTCTC	2262
Qy	2335	TTAAACCTCGTGCATCACTGCTGTGCCACTGTGACGAGCTCAATTACTCTCTGTGGGCTG	2394
Db	2263	CTTGTCTTTGCCATGGCCATTACAGCGCTGTCTTCTTCTCCAAACATCATCAGACTGCCCC	2322
Qy	2395	GATGCTCCCTGTGTGAGGGCACCATGCCCAACCTGCAGCTTCTCCTGAGTACTTCACTCGGG	2454
Db	2323	TTCCAGACTCCCCAATGTGTCTTCCATGAATTTCCAAACCTCTCTGTGGGAGCTCCCTGGGTCT	2382
Qy	2455	AACATGCTGTGAGTCTCTTTGGGCAGCTCTGTCTTCTCTGCACATCAAGCAGCATCGGGAAG	2514

US-10-282-942-1
; Sequence 1, Application US/10282942
; Publication No. US20030087295A1
; GENERAL INFORMATION:
; APPLICANT: siloes-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITILE OF INVENTION: TREATMENT AND DIAGNOSIS OF PAIN DISORDERS USING 9805
; FILE REFERENCE: MP101-240P1RM
; CURRENT APPLICATION NUMBER: US/10/282,942
; PRIORITY FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,047
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6196
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-282-942-1
Query Match 13.9%; Score 493; DB 15; Length 6196;
Best Local Similarity 49.8%; Pred. No. 1.9e-129;
Matches 1586; Conservative 0; Mismatches 1515; Indels 84; Gaps 10;
QY 417 GTACAGCGGTACTCTTCCAGATGAACACAGAGCAGCCTGACGCTGCTGATGCGGTGCT 476
Db |||||
QY 477 GGTGCTGTACAGCGGTGCTGCTGCTTTCACGCGCACCGCGCCCTCAGCCTGC 536
Db |||||
QY 397 TGCCTGCGTGGCCCTCATCATCATGCTTCAGCCAGGCGGACCCCTCCAGACACACGCG 456
QY 537 CTATGTGGCACTGTGGCTGTGCGCGCCCTGTTGCTGGGGCTCATGCTGTGTAA 596
Db |||||
QY 457 CATCTGGGCATGGGCTTCTGCTGCTGGCGGTGTTGGCGCCCTCTCTGCTGATGA 516
QY 597 CCGGCATAGCTTCCGCCAGGACTCCATGTGGTGTGATGATGATGCTGGGCATCCT 656
Db |||||
QY 517 CGTCAGTGTCTCTCGCGCGCTGCTCAGGCGCTTGGCGCTGCTCACCCTGGCGCTGTT 576
QY 657 GCGCGCAGTGCAGGTGCGGGCGCTCTGCAGCAGACCGCGCGCCCTCTGCG- GCGC 715
Db |||||
QY 577 GGTGCGCTGGGCTATGTGCTGCTGTTCAGCATGGAACAAAGGCGCGCTGTGCGTGGGA 636
QY 716 TCTGTGCGCCT-----GTGTTCTTTGTCTACATCGCTACAGCTCCTCCCATCCGAT 770
Db |||||
QY 637 GCAGTGGCCTTCTTCTCTGTTCTTCTGCTGTGTGTACACACTACTGCCCCCTCAGCAT 696
QY 771 GCGGCTGCGCTCTCAGCGGCTGGGCTCTCCACCTTTGCAATTTGATCTTGGCCTGGCA 830
Db |||||
QY 697 GCGGCGCTGTGCGCGTGGGCGCTCTCCACTGCTCCACCTCCCTGCTGCTGCTGCTC 756
QY 831 ACTTAACGCTG-----TGATGCTTCTCTGGAAGAGCTGCGTGGCCATGT 878
Db |||||
QY 757 TTTGATGGAGGCTTTCAGCACCCAGTGTTCGCGGTGGGCTGCGAGCTGCTGCGCAACGC 816
QY 879 GCTGCTGTTCTCTGCACCAAGTCAATGGCATCTGCAACACTATCCAGCAGAGGTGTC 938
Db |||||
QY 817 AGTCATCTTCTGTTGGGAACCTGACAGCGCCCTTCCAAAGCACCAATGCGAGTGC 876
QY 939 TCAGCGCCAGGCTTTTCAGGAGACCGCGTTTACATCCAGGCGCGGCTCCACCTCAGCA 998
Db |||||
QY 877 GTCCCGGACCTTTCACCTACATGTGAAGTGATCCAGATCCCGCGAGCTCGCAT 936
QY 999 TGAGAACTCGGAGCAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1058
Db |||||
QY 937 CGAGAAGCGCCAGCAGGAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 996
QY 1059 GATGAAAGAGACATCAACACAAAAAGAA-----GA 1091
Db |||||
QY 997 CATGAAGCTGGCCATCATCGAACGGCTCAAGGAGCATGGTACCGTGTGATCGCTGA 1056
QY 1092 CATGATGTTCCAAAGATCTACATACAGAAAGCATGACAATGTGTCAGCATCTCTGTTGCAGA 1151

Db |||||
QY 1057 CAACAACTTCCACAGCCTCTACGTCAAGAGGACCCAGAATGTGACATCTCTATGCGGA 1116
QY 1152 CATTGAGGCTTCCACAGCCTGGCATCCAGTGCATCTGGCAGGAGCTGCTCATGACCT 1211
Db |||||
QY 1117 CATCTGGGCTTCCAGCAGCTGGCAGGACTGTTCTCCAAAGAGCTGCTGCTGCTGCT 1176
QY 1212 GAATGAGCTCTTTGCGCGGTTTGACAAAGCTGGCTCGGAGAAATCACTGCTCAGGATCAA 1271
Db |||||
QY 1177 GAATGAGCTCTTTGCGCAAGTTTCGACCATCGCAAGGCCAACGAGTGCATGCGAATCAA 1236
QY 1272 GATCTGGGAGACTCTTACTACTGTGTCTGAGGCTGCGGAGGCCCGGCGCGCATGTC 1331
Db |||||
QY 1237 GATCTCTGGGAGCTGCTACTACTGTGTATCGGCGCTGCGCGTGTGCTGCTGCTGCTG 1296
QY 1332 CCACCTGCTGTGGAGATGGGGGTAGACATGATGAGGCCCATCTCGCTGGTGTGAGGT 1391
Db |||||
QY 1297 CCGGAACTGCGTGAAGATGGGGCTGGACATGTGCCAGGCGCATCAAGCAGGTGCGGAGGC 1356
QY 1392 GACAGGTGTGAATGTGAACATGCGGCTGGGATCCACAGCGGCGCGCTGCACTGCGGCT 1451
Db |||||
QY 1357 CACGGGCTGGACATCAACATGCGTGTGGGATACACTCGGGGAATGTGCTGCGGGGT 1416
QY 1452 CTTGGCTTGGGAAATGGCAGTTGCTGATGTGTGCTCAATGATGACCTTGGGCAACCA 1511
Db |||||
QY 1417 CATCGGCTGGCAGTGGCAGTATGAGTGTGTGCTGCCACGACGTGCTCCCTGGCCAAACG 1476
QY 1512 CATGGAGCAGGAGGCGCGGCTGCGCGCATCCACATCACTCGGCGCAACACTGCACTCT 1571
Db |||||
QY 1477 GATGAGGACGCCCGGAGTACCGCGCGGTGCACATCAAGAGGCGCACGCTAAAGACCT 1536
QY 1572 GAAACGCGGACTACAGAGTGGAGCCAGGCGCTGCTGGCGAGCCAGCAACGCTACTCAAGA 1631
Db |||||
QY 1537 GGAACAGGCTTACAGGTTGGAGATGGGCAAGGCGAGCAGCGGACCTCTACTCAAGGA 1596
QY 1632 GACGACATGAGACTTTCTCTCATCTTGGGCGCCAGCCAGCAAAACGGAAGAGGAGAGGC 1691
Db |||||
QY 1597 GATGAACATCCGACCTACCTGGTTCATCGACCCCGGAGCCAGCAGCACCCTCCCGCAG 1656
QY 1692 CATGCTGCGCAAGCTGACGCGACTGCGGCGCACTCCATGGAAGGCTGATGCGCGCTG 1751
Db |||||
QY 1657 CCAACACCTCCCGAGGCCAAGGGGAGCGCGGCTGGAAGATGCGGGGCTCAGTGCAT 1716
QY 1752 GGTCTCTGATGCTGCTTCTCCCGGACCAAGGACTCCAAAGGCTTCCGCGCAGATGGCAT 1811
Db |||||
QY 1717 GACCGGTACTCTGAGTCTCTGGGGGCGGCGACGCGCTTTCACATCTCAACCAACGGA 1776
QY 1812 TGATGATTCAGCAAAAGCAACCGGGGCAACCAAGATGCTCCGAACTCTGAGGATGAGGT 1871
Db |||||
QY 1777 GAGCTGAGCAGTGTGTGAGACCCAGCTCCCAACGCGGCGAGGCTTAAGAGCGTTCCCA 1836
QY 1872 GGATGAGTTCCTGAGCGCTGCTGATGCGCGGAGATTTGATGAGCTGCGGAGGACCA 1931
Db |||||
QY 1837 GCGCCACCGCGGAGCCCGCAGACAGAGCATGTCCCCAAGGGGCGGTGCGGAGGATGACTC 1896
QY 1932 TGTGCGCGGTTCTGCTCACCCTTCCAGAGAGGATCTTGAAGAGAGTACTCCCGGAA 1991
Db |||||
QY 1897 GTACGATGACAGATGCTGTGAGCCATTTGAGGGCTGAGCTCCAGAGGCGCTGCTGCTC 1956
QY 1992 GGTGATCCCCGCTTGGAGGCTTACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2051
Db |||||
QY 1957 CAACTCCGATGACTTCTACACCTTTGGGTTCATCTCTCGGAGAGGCTTTGAGCGGA 2016
QY 2052 CTTTCATCAGGCTTCTCATCTTCCACACTCCACCTGATGCTTGGGATCTATGCCAGAT 2111
Db |||||
QY 2017 GTACCGCTGCGACCCATCCCGCGGCGCGCAGACTTTGCTGCTGCGGCGAGCTGATCTT 2076
QY 2112 CTTCTGCTGCTGCTTAATCACCGTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2171
Db |||||
QY 2077 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2134
QY 2172 CCCTAAGGCCCTCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2231

Db 2135 TCCTTCGGGCTGTGGGCTGTGTACTGGGGC-TGGTCTGGGCTGTGCTTTGGCCACCA 2193
Qy 2232 AGTTGGCATCTTTTCGGTCTGCTGTGTACTTCTGCGCATTCGCCAACAATGTTACCTG 2291
Db 2194 GTTCTCGAGTGTCTGCCAGCTCGGGGAGCGCTCTGCACATCTCTGAGAGGTGGAGAC 2253
Qy 2292 TAACCAACACCCCATACGGAGCTGTGACGCCGGA-----TGCTGAATTTAAC 2339
Db 2254 ACAGCCCTCTGTAGGCTGACCCCTGGCGCTCTGACCATCGGCAGCCCTGCTCACTGTGGC 2313
Qy 2340 ACCTGCTGACATCACTGCCCTGCACCTGCAGAGCTCAATTAATCTCTGCGGCTGTGATGC 2399
Db 2314 CATCATCAACCTGCCCTGATGCCCTTTTCCAAGTTCCAGAGCTGCTGTGGCAATGAGAC 2373
Qy 2400 TCCCTGTGTGAGGACCAATGCCACCTGCAGCTTTCCTGAGTACTTCATCGGACAT 2459
Db 2374 AGGCTACTGGCGGAGCAGCAAGACAAGAGCCCTGTGTAGCCCTCTCCCGTACTAC 2433
Qy 2460 GCTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTCTGCAATCAGCAGCATCGGGAAGTTGGC 2519
Db 2434 CTGCAGCTGTCTCTGGCTTCATCGCTCTCTGGTCTTCTGAGGATGAGCCCTGGAGCC 2493
Qy 2520 CATGATCTTTGCTTGGGGCTCATTAATTTGGTCTGCTTCTGCTGGGTCCTCCAGCCAC 2579
Db 2494 AAAGTTGTCTGCTGACAGTGGCCCTGTGTGGCTACCTGCTGTCTTCAACCTCTCCCC 2553
Qy 2580 CATCTTTGACAACTATGACCTACTGCTTGGGTCCTAGCTTGGCTTCTTCCATGAGAC 2639
Db 2554 ATGCTGGCATGGGACTGCTGCGGCCAAGCCCTGGGCAACCTCACCAAGCCCAAGCCAC 2613
Qy 2640 CTTTATGATGGCTGACCTGCTCAGCTGACGGAGGGTGGCCCTCAAATATATGACCCCTGT 2699
Db 2614 CACCACTGG-----CACCCCTAGCTTCTCTGGAAGGACTGAGACCATGACCAATTT 2667
Qy 2700 GATTCCTGCTGGTGTGGCTGTGCTGTATATCTGATGCTCAGCAGTGTGAGTGCATGC 2759
Db 2668 CTACCTGGCTGTCTTACATCACTACCTGCTTACACTCTCCAGACAGATTGACTATTACTG 2727
Qy 2760 CCGCTTAGCTTCTCTGGAACCTACAGGCAACAGGGGAGGAGGAGATGAGGAGCT 2819
Db 2728 CCGCTTGGACTGCTCTGGAAGAAAGTTCAAGAGGAGCAGAGGAGTTTGAACCAT 2787
Qy 2820 ACAGGCATACAAACCGGAGGCTGTGCTAATACTTCTGCCAAGGACGTGGCGGCCACTT 2879
Db 2788 GGAGAACGTGAACCGCTTCTCTGGAGAACGCTCTGCCAGCCACGTGCTGCCACTT 2847
Qy 2880 CTTGGCCCGGAGCGCGCAATGATGAATCTTACTATCACTGTGTGAGTGTGTGGCTGT 2939
Db 2848 TATCG---GTGACAAAGTTAAACGAGGACTGCTACCATCACTTATGACTGCGTCTGTGT 2904
Qy 2940 TATGTTTGCCTCCATTGCCAATCTCTGAGTTCTATGTGGAGCTGGAGGCAACATGA 2999
Db 2905 CATGTTTGCCTCGCTGCGGACTTCAAAGTGTCTACAGAGTGGCATGTCAACAAGA 2964
Qy 3000 GGGTGTGCTGCTGCGGCTGTCAACAGATCATCGCTGACTTTTGTATGAGATTAATCAG 3059
Db 2965 AGGCTGAGTGTGCTAGCTGTCTCAATGAGATCATTTGCCGACTTTCAGCAGCTCTACT 3024
Qy 3060 CGAGGAGCGGTTCCGGCAGCTGGAATAAGATCAAGACGATTTGGTAGCACTTACATGGCTGC 3119
Db 3025 GAAGCCCAAGTTACGCGCGTGGAGAGATCAAGACCCTCGGACACGTCATATGCGAGC 3084
Qy 3120 CTAGGGCT-----GACGCCAGCACCTACGATCAGTGTGGGCGCTCCCA 3164
Db 3085 TGCAGGGCTCAGCGTCCGCTCAGGGCACAGAACCGAGGACTGGAGCGGACGATGCCCA 3144
Qy 3165 CATCACTGCTGCTGACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3224
Db 3145 CATTTGTTGATGTTGAGTTCAGCATCGCCCTCATGAGTAAGTGTGAACGATCAACAG 3204
Qy 3225 GCATCTCTTCAACAATTTCCAGATGAAGATTTGGGCTGAAATGGGCCCTGCTGTGGCAGG 3284
Db 3205 GCATCTCTTCAACTCTTCCGCTTCCGCTCGGCTAAACCATGCGGCTGTGTGTTGCTGG 3264

Qy 3285 TGTATCGGGGCTCGAAGCCACAGATATGACATCTGGGGGAAACACAGTGAATGTCTTAG 3344
Db 3265 AGTATTTGGGCCCCGAAACCTCAGTATGACATCTGGGGAACACATGTCAATGTGGCAG 3324
Qy 3345 TCATATGAGACAGCACCGGGGTCCCCACCGAATCCAGGTGACCAACGACCTGTACCAAGT 3404
Db 3325 CCGAATGGAAGCACTCGGAGAACTTGGGAAATCCAGGTTACCGAGGAGACCTGCACCAT 3384
Qy 3405 TCTAGCTGCCAAGGGCTACAGCTGAGTGTTCAGGGGTGCTCAAGGTGAAGGCAAGGG 3464
Db 3385 CTCCAGGGCTCTCGGTACTCTTTGTAATGCCGTGGCTGTCAACGTTCAAGGCAAGG 3444
Qy 3465 GGAGATGACCAACCTACTTCTCAATGGGGCCCCCAGCAGTTAACAGGCCCCCAGCCACAA 3524
Db 3445 CGAGCTGAGGACTTACTTTTCTGTAGGACACTGCGCAGTTTCAGGGGCTGGGGCTGAA 3504
Qy 3525 TTCAG 3529
Db 3505 CTGAG 3509

RESULT 13

US-09-960-706-635
; Sequence 635, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960, 706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 635
; LENGTH: 2731
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 L05500
US-09-960-706-635

Query Match 12.8%; Score 456.2; DB 13; Length 2731;
Best Local Similarity 52.8%; Pred. No. 4.2e-119;
Matches 1274; Conservative 0; Mismatches 1023; Indels 114; Gaps 9;

Qy 1090 GACATGATGTTCCACAAGATCTACATACAGAACATGACAAATGTACGATCCTGTTTGA 1149
Db 24 GAGAGGATTTTCCACAAGATTTATATCCAGAGGACGACAAATGTAGCATCTCTGTTGCT 83
Qy 1150 GACATGAGGGCTTCCAGGCTGCGCATCCAGTGCATCGCAGGAGCTGTGATGACC 1209
Db 84 GACATGAGGGTTTACAGGGCTTGGCATCCAGTGCACAGCCAGGAGCTGTGTAACCTC 143
Qy 1210 CTGAATGAGCTCTTTGCCCGGTTTGAAAGCTGGCTGCGGAGAAATCACTGCTGAGGATC 1269
Db 144 CTCAATGAGCTCTTTGGCAAGTTTCGATGAATTAGCCAGCGAGAAACCACTGTCGCGCATC 203
Qy 1270 AAGATCTTGGGGACTGTTACTACTGTGTGTCAGGGCTGCGGAGGCCCCGGGCGGACCAT 1329
Db 204 AAGATCTTGGGGACTGCTACTACTGCTGTGTGCGGGCTTACCAGGCCCAAGACTGACCAT 263
Qy 1330 GCCCACTGCTGTGAGATGGGGTAGACATGATTGAGGCCATCTGCTGTTGACGTGAG 1389
Db 264 GCCCACTGCTGTGAGATGGGACTGACATGATGTTGATACCATCACTCTGTGGCTGAA 323
Qy 1390 GTGACAGGTGTGAATGTGAACATGCGCGTGGGCAATCCACAGCGGCGGCTGCACTGCGGC 1449

Db 324 GCCACGAGTGGATCTGAACATGCGGTGTGGGTCTGCACACGCGGACAGGTCTCTGTGGT 383
Qy 1450 GTCTTTGGCTTCGGAAATGGCAGATTTCGATGTGTGTCCTCAATGATGACCTTCGGCCAA 1509
Db 384 GTCTGGGCTTCGGCAAGTGGCAGTACGACGTGTGTCCATGATGTGACCTTGGCCAT 443
Qy 1510 CACATGGAGCAGAGGCGCGGTGGCCGATCCACATCACTTCGGGCAACATTCGAGATAC 1569
Db 444 GTCATGGAACCGCTGGCCCTGCAGGGAAGGTTCATATCACAAAGACGACCTTAGCGTGC 503
Qy 1570 CTGAACGGGGACTACGAGGTGAGCCAGGCGCGTGTGGGAGCGCAAGCGTACCTCAAG 1629
Db 504 TTGAATGGGAGCTACGAGGTAGAACCGGTTACGGACATGAGAGGAACAGTTTCTTGAAA 563
Qy 1630 GAGCAGCACATTTGAGACTTTCTCTCTCTGGGCGCCAGCCAGAAACGGAAGAGGAGAG 1689
Db 564 ACTCATAAATCGAAACCTTTTATTTGTGCCATCCATCGCGGAAGATATTTCCAGGC 623
Qy 1690 GCATGCTGGCAAGCTGACGGGACTCGGGCAACTCGGGCACTCATGGAAGGGGTGATGCGGCG 1749
Db 624 CTGATTTCTCTAGATATAAACC-----GGCCAAAGGATGAAGTTCTAGACTGTCTGC 677
Qy 1750 TGGGTTCTGTGATCTGCTCTCTCCGGACCAAGGACTCCAAAGGCTTGGCCAGATGGGC 1809
Db 678 TACCTGTGTGAGCTCATGCACTCCCGAATAATGTTCAAGCCGAGATCCCTTCTCC 737
Qy 1810 ATTGATGATTTCCAGCAAGACAAACCGGGCACCAAGATGCCCTGAACCTCAGGATGAG 1869
Db 738 AATGTCATGACCTCGGAGGACGA-----TGAGAACGGAGGCG 775
Qy 1870 GTGGATGAGTTCTGAGCGGTGCCATTCGATGCGCGAGCAATTCATGAGTGGGAGGAC 1929
Db 776 ATTAAGAACAGCTCGGAAAACTCAGAAACCGCTCATCTTTTCTACCAAG----- 828
Qy 1930 CATGTGGCGCGTTCTGCTCACTTCCAGAGAGGAGTCTTGAGAGAGTACTCCCGG 1989
Db 829 -----TTGTACACCAACCCCGGCACTCGCGTCAACAGGTACATCAGCCGC 875
Qy 1990 AAGTGGATCCCGCTTCGGAGCTACGTTGCTGTGCTGCTGTGCTTCTGCTTCATC 2049
Db 876 CTCCTTAGAACCCCGCAGACAG---AGCTGGAGATGGCAGACCTGAACTTCTTACCTCG 932
Qy 2050 TGCCTCATCCAGTCTCATCTTCCACACTCCACCCTGATCTTGGGATCTATGCCAGC 2109
Db 933 AAGTACAAACATGTCCGACGGAGCAAAAGTACCACAGCTTCAGGACGAGTATTTACC 992
Qy 2110 ATCTTCTGCTGCTGCTAATCACCGTGTGATCTGTGCTGTGCTACTCTGCTGCTGTCTG 2169
Db 993 AGCGCGTTGCTCCTCACCTCATCTGCTGCTGCTTTATTTGGCTTGTCTTACCTCTAATA 1052
Qy 2170 TTCCCTAAGGCGCTGCAACGCTGTGCTCCGACAGATTGTCGCTCAGGGSCATAGCAC 2229
Db 1053 TTCCACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1112
Qy 2230 GCAGTTGGCATCTTTTCCGCTGCTGTGTTTACTTTCGCAATTCGCCAATGTTTACC 2289
Db 1113 TGTGTCTGTACTGTCACATCACCCGGGT-----CCAGTGTTTTCCAGGCTGCC 1161
Qy 2290 TGTATACCACACCCCATACGAGCTGTGACGCGCGGATGCTGAATTTAATCCTGCTGAC 2349
Db 1162 TGACGATTCAGATTGCGACTGCTGCTGTGTTTATTTTATAGTGTGCTTAACTACTCAGTAG 1221
Qy 2350 ATCACTGCTGCGACTGCGAGCAGCTCAATTACTCTCTGGGCTGGATGCTCCCTGTGT 2409
Db 1222 CCCAAG-----TTGTGTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1271
Qy 2410 GAGGCAACCATCCCACTGACGCTTCTCTGAGTACTTTCATCGGGAACATGCTGCTGAGT 2469
Db 1272 AACAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1331
Qy 2470 CTCCTTGGCAGCTCTGCTCTTCTGACATCAGCAGATCGGGAAGTGGCCATGATCTTT 2529
Db 1332 TGCAGTCTACACACCATGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1391

RESULT 14
US-09-925-297-352
; Sequence 352, Application US/09925297

Qy 2530 GTCTTGGGCTCATCTATTTGGTGTGCTTCTGTGGGTCCCCAGCCACCATCTTTGAC 2589
Db 1392 TTTTTCGGGTGCTCTCTCTTCCAAAATGATCTCTGCTCTCGGGCTCACACAGCTCTAC 1451
Qy 2590 AACTATGACCTACTGCTTGTGGGTGCATCGCTTGGTCTTCTTCCAATGAGACCTTTGATGG 2649
Db 1452 ATCTCTGCTTGGAGCTCAGCGGATACACAGGAC----- 1486
Qy 2650 CTGGACTGTCCAGCTGCAGGGAGGGTGCCTCAATATATGACCCCTGTGATTTGCTG 2709
Db 1487 -----TGGGGTGTGCTGCTCTCCGGGCGCAGCTACGAGCCGATTTGTGGCCATCTCTG 1538
Qy 2710 GTGTTTGGCTTGGCCCTGTATCTGCACTCAGCAGGTGGAGTGCACCTGCCCGCTTAGAC 2769
Db 1539 CTCCTTCTCTGTGGCTGCGCTGATCCAGGCAAGTGGACATCAGGCTGAGGCTGGAC 1598
Qy 2770 TTTCTCTGGAACATACAGGCAACAGGAGAGAGGAGAGATGAGGAGCTACAGGCATAC 2829
Db 1599 TACCTCTGGGCGGCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1658
Qy 2830 AACCGAGGCTGTGCATTAACATCTGCCCAGGAGCTGGGCGCCACTTCTGCGCCCG 2889
Db 1659 AACAGGCGATCTCTTCAACCTCTGCGGCGCAGCTGCGCCAGCATCTTCTCATGTCC 1718
Qy 2890 GAGCGCCCAATGATGAACCTCTACTATCAGTGTGTGAGTGTGTGGCTGTTATGTTTGC 2949
Db 1719 AACCTCTCGAATGAGCACTCTACTACAGTCTTACTCCAGTGGGCTCATGTTTGC 1778
Qy 2950 TCCATTGCGCACTTCTCTGAGTTCATGTGAGCTGGAGGCAACAAATGAGGCTGTGAG 3009
Db 1779 TCCATCCCAACTTCAATGACTTCTACATCAGCTGGAGCGGCAACAAATGAGGCTGGAG 1838
Qy 3010 TGCCTGCGGCTGTCAACGAGATCATCGCTGATTTGATGAGATTTATCAGCGAGGCGG 3069
Db 1839 TGTCTGCGGCTTCTCAACGAGATCATCGCCGACTTTTGAAGGCTCATGGAAAAAGACTTT 1898
Qy 3070 TTCCGGCAGCTGGAAAAAGATCAAGACGATTTGTAGCCTTACATGCTGCTCAGGGCTG 3129
Db 1899 TACAGGACATAGAGAGATCAAGACCATCGGAGCATTACATGCTGCTGCTGCTGCTGCTG 1958
Qy 3130 AACGCG-----AGCACCTACGATCAGGTGGGCGCTCCCATCATCTGCTGCTGCT 3180
Db 1959 GCGCCCACTCGGGGACCAAGGCTAAGAGTCCATCTCTCCACCTGAGCAGCTGGCG 2018
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RESULT 15

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; Sequence 4198, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4198
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; LENGTH: 463

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(463)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-4198
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Best Local Similarity 93.4%; Pred. No. 9.1e-102; Mismatches 29; Indels 1; Gaps 1;

Matches 422; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3545.6	99.8	4942	US-09-474-076-1	Sequence 1, Appli
2	3484.8	98.1	3549	US-09-008-097-5	Sequence 5, Appli
3	3051.2	85.9	4046	US-07-793-961A-1	Sequence 1, Appli
4	3051.2	85.9	4046	US-08-240-357-1	Sequence 1, Appli
5	2810.4	79.1	4131	US-08-726-214-11	Sequence 11, Appli
6	1763.4	49.6	1812	US-09-008-097-3	Sequence 3, Appli
7	1761	49.6	4523	US-09-473-716-1	Sequence 1, Appli
8	1696.2	47.8	3924	US-08-726-214-9	Sequence 9, Appli
9	604.4	17.0	3978	US-08-726-214-1	Sequence 2, Appli
10	512.4	14.4	3518	US-09-412-210-2	Sequence 2, Appli
11	485.2	13.7	4601	US-08-726-214-15	Sequence 15, Appli
12	458.6	12.9	4008	US-08-307-896-5	Sequence 5, Appli
13	458.6	12.9	4008	US-08-726-214-3	Sequence 3, Appli
14	458.6	12.9	4008	US-08-726-214-3	Sequence 5, Appli
15	456.2	12.8	2731	US-09-016-434-1344	Sequence 1344, Ap
16	455.4	12.8	4533	US-08-726-214-5	Sequence 5, Appli
17	449.4	12.7	5199	US-08-726-214-13	Sequence 13, Appli
18	431	12.1	3357	US-08-726-214-7	Sequence 7, Appli
19	389.8	11.0	1652	US-08-726-214-17	Sequence 17, Appli
20	345	9.7	4079	US-09-016-434-1412	Sequence 1412, Ap
21	295.2	8.3	314	US-09-008-097-1	Sequence 1, Appli
22	293	8.2	2092	US-08-307-896-6	Sequence 6, Appli
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24	227.4	6.4	4473	US-08-894-173-1	Sequence 1, Appli
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26	218	6.1	4985	US-09-473-717-1	Sequence 1, Appli
27	216.4	6.1	5515	US-09-398-193-98	Sequence 98, Appli

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	31	66.6	1.9	1259	2	US-08-997-080-123	Sequence 123, App
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	34	66.6	1.9	1259	4	US-09-324-542-123	Sequence 123, App
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	36	66.6	1.9	2013	2	US-08-997-080-176	Sequence 176, App
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	41	66.6	1.9	2172	2	US-08-997-080-173	Sequence 173, App
	42	66.6	1.9	2172	2	US-08-997-362-173	Sequence 173, App
	43	66.6	1.9	2172	3	US-09-095-855-173	Sequence 173, App
	44	66.6	1.9	2172	4	US-09-324-542-173	Sequence 173, App
	45	66.6	1.9	2172	4	US-09-205-426-173	Sequence 173, App

ALIGNMENTS

RESULT 1
US-09-474-076-1
; Sequence 1, Application US/09474076
; Patent No. 6465237
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; FILE REFERENCE: 44481-5028-01-US
; CURRENT APPLICATION NUMBER: US/09/474,076
; PRIOR FILING DATE: 1999-12-12
; PRIOR APPLICATION NUMBER: PCT/US98/13694
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,904
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,550
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4942
; TYPE: DNA
; ORGANISM: human type VI adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(3648)
US-09-474-076-1

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1184

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RESULT 2
US-09-008-097-5
; Sequence 5, Application US/09008097
; Patent No. 6306830
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
; TITLE OF INVENTION: HEART FAILURE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,097
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dylan, Tyler M
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 22000-20567.21
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 5:
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; LENGTH: 3549 base pairs
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; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...3501
; OTHER INFORMATION:
US-09-008-097-5

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Matches 3517; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

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1498 CTGGCCAAACACATGAGAGCAGGAGCGGGCTGGCGCATCCACATCACTCGGGCAACA 1557
1561 CTGCACTTACCTGAAACGGGACTACGAGGTGGAGCCAGGCGGTGGCGAGCGCAACGCG 1620
1558 CTGCACTTACCTGAAACGGGACTACGAGGTGGAGCCAGGCGGTGGCGAGCGCAACGCG 1617
1621 TACCTCAAGAGCAGACATTTGAGACTTTTCTCATCTCTGGGCGCCAGCGCAAGAAACGAAA 1680
1618 TACCTCAAGAGCAGACATTTGAGACTTTTCTCATCTCTGGGCGCCAGCGCAAGAAACGAAA 1677
1681 GAGGAGAGGCCATGCTGGCCAGCTGACGAGCTCGGCGCAACTCCATGGAAGGGCTG 1740
1678 GAGGAGAGGCCATGCTGGCCAGCTGACGAGCTCGGCGCAACTCCATGGAAGGGCTG 1737
1741 ATGCCCGCTGGGTCTCTGATGTGCTTCTCCGAGCAAGGACTCCAGGCTTCCCGC 1800
1738 ATGCCCGCTGGGTCTCTGATGTGCTTCTCCGAGCAAGGACTCCAGGCTTCCCGC 1797
1801 CAGATGGGCATTTGATGATTTCCAGCAAGACAACCGGGGCAACCAAGATGCTTGAAGAAAG 1860
1798 CAGATGGGCATTTGATGATTTCCAGCAAGACAACCGGGGCAACCAAGATGCTTGAAGAAAG 1857
1861 GAGGATGAGGTGAGTTCCTGAGCGGTGCCATCGATCGCCGAGCATTTGATCAGCTG 1920
1858 GAGGATGAGGTGAGTTCCTGAGCGGTGCCATCGATCGCCGAGCATTTGATCAGCTG 1917
1921 CGGAAGACCATGTGCGCGCTTCTGCTCACCTCCAGAGAGAGGATCTTGAAGAAAG 1980
1918 CGGAAGACCATGTGCGCGCTTCTGCTCACCTCCAGAGAGAGGATTTGAAGAAAG 1977
1981 TACTCCGGAAAGGTGATCCCGCTTTCGAGAGCTAGCTTGCCTGTGCTTGGCTTTC 2040
1978 TACTCCGGAAAGGTGATCCCGCTTTCGAGAGCTAGCTTGCCTGTGCTTGGCTTTC 2037
2041 TGCTTCATCTGCTTTCATCCAGCTTCTCATCTTCCACACTCCACCTGATGCTTGGGATC 2100
2038 TGCTTCATCTGCTTTCATCCAGCTTCTCATCTTCCACACTCCACCTGATGCTTGGGAT 2097
2101 TATGCCAGCATCTTCTGCTGTCTGCTTAATCAACCGTGTCTGCTGTGTGTACTCTCTGT 2160
2098 TATGCCAGCATCTTCTGCTGTCTGCTTAATCAACCGTGTCTGCTGTGTGTACTCTCTGT 2157
2161 GGTTCCTGTTCCTTAAGGCCCTTGCAAGCGTCTGTCCGAGCATTTGTCCGCTCACGGGCA 2220
2158 GGTTCCTGTTCCTTAAGGCCCTTGCAAGCGTCTGTCCGAGCATTTGTCCGCTCACGGGCA 2217
2221 CATAGCAGCGAGTTCGCTTCTTTCCTGCTTCTGTTTACTTCTGCTTTCGCTTTCGCAAC 2280
2218 CATAGCAGCGAGTTCGCTTCTTTCCTGCTTCTGTTTACTTCTGCTTTCGCTTTCGCAAC 2277
2281 ATGTTTCACTGTAAACACACACCCCATACCGAGCTGTGCGAGCGGATGCTGAATTTAAACA 2340
2278 ATGTTTCACTGTAAACACACACCCCATACCGAGCTGTGCGAGCTGTGAGATTTAAACA 2337
2341 CTGCTGACATCACTGCTGCGCACTTTCAGAGCTCAATTTACTTCTCTGGGCTGGATGCT 2400

Db 2338 CCTGCTGACATCACTGCTGCTGCCACCTGCGAGAGCTCAATTACTCTCTGCGCCCTGGATGCT 2397
Qy 2401 CCCCTGTGTGAGGACCACTGCCCACCTGCACTTCTCTGAGTACTTCAATCGGGAAACATG 2460
Db 2398 CCCCTGTGTGAGGACCACTGCCCACCTGCACTTCTCTGAGTGTTCATCGGGAACATG 2457
Qy 2461 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGCGACATCAGCAGCATCGGGAAGTTGGCC 2520
Db 2458 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGCGACATCAGCAGCATCGGGAAGTTGGCC 2517
Qy 2521 ATGATCTTTGCTTGGGGCTCATCTATTGTTGGTGTCTTCTGCTGGTCCCGCCAGCCACC 2580
Db 2518 ATGATCTTTGCTTGGGGCTCATCTATTGTTGGTGTCTTCTGCTGGTCCCGCCAGCCGCC 2577
Qy 2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCCAATGAGACC 2640
Db 2578 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTGGCTTCTTCCCAATGAGACC 2637
Qy 2641 TTTGATGGCTGAGCTGCTCCAGCTGAGGAGGGTGGCCCTCAATATATATGACCCCTGTG 2700
Db 2638 TTTGATGGCTGAGCTGCTCCAGCTGAGGAGGGTGGCCCTCAATATATATGACCCCTGTG 2697
Qy 2701 ATTCTGCTGCTTTGCGCTGGCTGTATCTGCAATGCTCAGCAGTGGAGTGCAGTGC 2760
Db 2698 ATTCTGCTGCTTTGCGCTGGCTGTATCTGCAATGCTCAGCAGTGGAGTGCAGTGC 2757
Qy 2761 CGCTAGACTTCTCTGGAACCTACAGGCAACAGGGGAGAGAGAGATGAGGAGCTA 2820
Db 2758 CGCTAACTTCTCTGGAACCTACAGGCAACAGGGGAGAGAGAGATGAGGAGCTA 2817
Qy 2821 CAGGCAATACACCGAGGCTGCTGATTAACATTTGCCCCAAGGAGTGGCGGCCCACTTC 2880
Db 2818 CAGGCAATACACCGAGGCTGCTGATTAACATTTGCCCCAAGGAGTGGCGGCCCACTTC 2877
Qy 2881 CTGGCCCGGAGCGCGCAATCATGACTCTACTATCATGCTGTGTGAGTGTGCTGTT 2940
Db 2878 CTGGCCCGGAGCGCGCAATCATGACTCTACTATCATGCTGTGTGAGTGTGCTGTT 2937
Qy 2941 ATGTTTGGCTCCATTGCCAATCTCTGAGTTCTATGTGGAGCTGGAGGCAACAACTAG 3000
Db 2938 ATGTTTGGCTCCATTGCCAATCTCTGAGTTCTATGTGGAGCTGGAGGCAACAACTAG 2997
Qy 3001 GTGTGAGTGTCTGCGGCTGCTCAACGAGATCATCGTGAATTTGATGAGATTAATCAGC 3060
Db 2998 GTGTGAGTGTCTGCGGCTGCTCAACGAGATCATCGTGAATTTGATGAGATTAATCAGC 3057
Qy 3061 GAGGAGCGGTTCCGCGAGCTGAAAGATCAAGAGATTTGTAGCACCTACATGCTGCC 3120
Db 3058 GAGGAGCGGTTCCGCGAGCTGAAAGATCAAGAGATTTGTAGCACCTACATGCTGCC 3117
Qy 3121 TCAGGCTGAAGCCAGCACTTACGATCAGTGGGCGGCTCCACATCACTGCGCTGGCT 3180
Db 3118 TCAGGCTGAAGCCAGCACTTACGATCAGTGGGCGGCTCCACATCACTGCGCTGGCT 3177
Qy 3181 GACTACGCCATCGGCTCATGAGCAGATGAAGCACAATGAGCACTCTTCAACAACT 3240
Db 3178 GACTACGCCATCGGCTCATGAGCAGATGAAGCACAATGAGCACTCTTCAACAACT 3237
Qy 3241 TTCCAGATGAAGATTGGGCTGAACATGAGGCGGCTGAGGAGTGTCTGCGGCTCGG 3300
Db 3238 TTCCAGATGAAGATTGGGCTGAACATGAGGCGGCTGAGGAGTGTCTGCGGCTCGG 3297
Qy 3301 AAGCACAAGTATGACATCTGGGGGAAACAGTGAATGTCTCTAGTCTGATGAGCAGCAG 3360
Db 3298 AAGCACAAGTATGACATCTGGGGGAAACAGTGAATGTCTCTAGTCTGATGAGCAGCAG 3357
Qy 3361 GGGTCCCGCAGCAATCCAGGTGACCGGACCTGTACCGAGTTCTAGCTGCCAAGGCG 3420
Db 3358 GGGTCCCGCAGCAATCCAGGTGACCGGACCTGTACCGAGTTCTAGCTGCCAAGGCG 3417
Qy 3421 TACAGCTGAGTGTGAGGGGTGTCAAGGTGAAGGGCAAGGGGAGATGACCACTTAC 3480
Db 3418 TACAGCTGAGTGTGAGGGGTGTCAAGGTGAAGGGCAAGGGGAGATGACCACTTAC 3477

Qy 3481 TTCTCTCAATGGGGGCCCCAGCAGTTTAAACAGGGGCCAGCCACAAAATTCAGCTGAAGGGACC 3540
Db 3478 TTCTCTCAATGGGGGCCCCAGCAGTTTAAACAGGGGCCAGCCACAAAATTCAGCTGAAGGGACC 3537
Qy 3541 AAGTGGGCACT 3552
Db 3538 AAGTGGGCACT 3549

RESULT 3

US-07-793-961A-1
; Sequence 1, Application US/07793961A
; Patent No. 5334521
; GENERAL INFORMATION:
; APPLICANT: Yoshihiro Ishikawa
; TITLE OF INVENTION: Cloning and Character-
; TITLE OF INVENTION: ization of a Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alan M. Gordon
; ADDRESS: American Cyanamid Company
; STREET: 1937 West Main Street,
; STREET: P.O. Box 60
; CITY: Stamford
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII from DW4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/793,961A
; FILING DATE: 19911118
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203 321 2719
; TELEFAX: 203 321 2971
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs listed
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-793-961A-1

Query Match 85.9%; Score 3051.2; DB 1; Length 4046;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 3260; Conservative 0; Mismatches 283; Indels 9; Gaps 3;

Qy 1 ATGTCATGTTTGTAGTGGCTCTCTGCTCCCTAAAGTGAAGTAAACGAAACAGCCCTGGGGT 60
Db 131 ATGTCGTTGTTTGTAGTGGCTCTCTGCTCCCTAAAGTGAAGTAAACGAAACAGCCCTGGGGT 190
Qy 61 GAACGCAATGGGAGAGAGCGTTCCGCGCGCGCTGGCACTCGGGGAGGTGGCTTCTGCACG 120
Db 191 GAACGCAATGGGAGAGAGCGT---CCAGCGCGCGGAGCTCGGACCCAGTGGCTTCTGCACG 247
Qy 121 CCCGCTATATGAGTGGCTCCGGGATGCGAGCCACCCAGCCCTGCGGGCCCC 180
Db 248 CCCGCTATATGAGTGGCTCCGGGATGCGAGCCCTGCGAGCCCTGCGAGCTCCCTGCGGCTCCC 307

Qy 181 CCTCGGTGCCCTGCGAGGATGACGCTTTCATCCGAGGGGCGGCCAGGCAAG 240
Db 308 CCTCGGTGCCCTTGGCAGGATGAGCCCTTCATCCGAGAGCGCGCCCGCAAGGGCAG 367
Qy 241 GAGCTGGGGGTGCGGGCAGTGCGCCCTGCGCTTCAGAGATACCGAGGTGAACAACGACGG 300
Db 368 GAGCTGGGGGTGCGGGCAGTGCGCCCTGCGCTTCAGAGATACCGAGGTGAACAACGACGG 424
Qy 301 GGGCGGACGCTGAGGTGGCGCGCGCGAGCGGTGCCAGGAGTGGCGCATCTCTGTGGCG 360
Db 425 GTTGGGGCAGCTGAGGTGGCCCTGACGTGACCCCGGGAGTAGCGCATCTCTGTGGCG 484
Qy 361 CGTCTGGTGCAGGTGTTCCAGTCCGAGCAGTTCCTGGTCCGACAGCTGGAGCGCTGTAC 420
Db 485 CGTCTGGCCCAAGGTGTTCCAGTCCGAGCAGTTCCTGGTCCGCAAGCTGGAGCGCTGTAC 544
Qy 421 CAGCGGTACTTCTCCAGATGAACACAGAGCAGCTGACGCTGCTGATGGCGGTGCTGGTG 480
Db 545 CAGCGGTACTTCTTCCAGATGAACACAGAGCAGCTGACGCTGCTGATGGCGGTGCTGGTG 604
Qy 481 CTGCTCAGCGGTGCTGGCTTCCAGCGCGCACCCCGCGCTCAGCGCTGCTAT 540
Db 605 CTGCTGACAGCGGTGCTGACGCTTCCAGCTGCTGACCTGCGCGCTCAGCGCTGCTAT 664
Qy 541 GTGCACTGTTGGCCCTGCGCGCGCCCTGTTCTGTTGGGGCTCATGTGTGTGTAAACCG 600
Db 665 GTGCGCTGCTGGCCCTGCGCGCACCCCTCTCTGTGCGCTCATGTGTGTGTAAACCG 724
Qy 601 CATAGCTTCGCGCAGGACTCATGTGGGTGGTGAATTAAGTGTGCTGGGATCTGTGGCG 660
Db 725 CACAGCTTTCGCCAGGACTCCATGTGGGTGTGAGCTACGTTGTGTGTGGGCTCTGGCA 784
Qy 661 GCAGTGCAGGTGCGGGCGCTCTCGAGAGACCGCGCGAGCCCTCTCGGGCGCTCTGG 720
Db 785 GCGCTTCAGGTGGGGGTGCGCTGGCAGCCAAACCCCGCAGCCCTCTGTGGGGCTCTGG 844
Qy 721 TGCCCTGTGTTCTTTGTCTATCGCTACACGCTCTCTCCCATCCGATCGCGGGCTGCC 780
Db 845 TGCCCTGTGTTTGTCTATCATCACCTACAGCTCTCTATCCCATCCGATCGCGGAGCT 904
Qy 781 GTCTCAGCGGCTGGGCCCTCTCACCTTGCAATTTGATCTTGGCTGGGCAACTTAACCGT 840
Db 905 GTCTTCAGTGGCCCTGGGCCCTGTCCACCTCGATTTGATCTTGGCTGGGCAACTCAACCG 964
Qy 841 GGTGATCCCTTCTCTGGAAGAGCTCGGTGCCAAATGTGCTGTCTCTCTGCAACCAAC 900
Db 965 GGTGACCCCTTCTCTGGAAGAGCTCGGTGCCAAATGTGCTGTCTCTCTGCAACCAAC 1024
Qy 901 GTCAATGGGCATCTGCACACTATCCAGAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 960
Db 1025 GTCAATGGGCATCTGCACACTATCCAGAGAGGTGTCTCAGCGCCAGGCTTTTCAGGAG 1084
Qy 961 ACCCGGGTTACATCCAGGGCCGGCTCCACTGCGAGCATGAGATCGGAGAGGAGCGG 1020
Db 1085 ACCCGGGTTACATCCAGGGCCGGCTGACCTGCGAGCATGAGATCGGAGAGGAGCGG 1144
Qy 1021 CTGCTGTGTCGTATTTGCCCGCCAGCATGTTGCCATGGAGATGAAGAAGACATCAACACA 1080
Db 1145 CTGCTGTGTCGTATTTGCCCGCCAGCATGTTGCCATGGAGATGAAGAAGATATCAACACA 1204
Qy 1081 AAAAAAGAAGACATGATGTTCCAAAGATCTACATACAGAGCATGACAAATGTGAGCATC 1140
Db 1205 AAGAAAGAAGACATGATGTTCCAAAGATCTACATCCAGAAGCATGACAAATGTGAGCATC 1264
Qy 1141 CTGTTTGCAGACATGAGGCGTTCAACAGCTGGCATCCAGTGCATCGCGCAGGAGCTG 1200
Db 1265 CTGTTTGCAGACATGAGGCGTTCAACAGCTGGCATCCAGTGCATCGCGCAGGAGCTG 1324
Qy 1201 GTCATGACCTGATGAGCTCTTTGCGCGTTTGACAAAGCTGCTCGGAGAAATCACTGC 1260
Db 1325 GTCATGACCTGAGCAGCTCTTTGCGCGCGTTTGACAAAGCTGCTCGGAGAAATCACTGC 1384
Qy 1261 CTGAGGATCAAGATCTTTGGGGGACTGTTACTACTGTGTGTGAGGGCTGCGGGGCGCG 1320

Db 1385 CTGAGGATCAAGATCTTAGGGACTGTTACTACTGTGTGCGGGCTGCGGAGGCGCGG 1444
Qy 1321 GCCGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATGATTGAGGCCATCTCGCTG 1380
Db 1445 GCAGACCATGCCACTGCGTGTGTGGAGATGGGGGTGAGACATGATGAGGCCATCTCGCTG 1504
Qy 1381 GTACGTGAGGTGACAGGTGGAATGTGAACATCGCGGTGGGCATCCACAGCGGGCGCGTG 1440
Db 1505 GTGCGTGAAGTGAACAGGTGTGAACATCCGCGTGGGCATCCACAGCGGGCGGTG 1564
Qy 1441 CACTGCGGGCTCTTGGCTTGGGAAATGGCAGTTGATGTGTGTGTTCCAAATGATGACC 1500
Db 1565 CACTGTGGTGTCTTGGCTTGGGAAATGGCAGTTGATGTGTGTGTTCCAAATGATGACT 1624
Qy 1501 CTGGCCAAACCATGAGGAGGAGCGCGGGCTGGCGGCATCCACATCACTCCGGGCAACA 1560
Db 1625 CTGGCCAAACCATGAGGAGGAGCGCGGGCTGGCGGCATCCACATCACTCCGGGCAACG 1681
Qy 1561 CTGCAGTACTGAAACGGGAGTACGAGGTGGAGCGCGGTGGCGGAGCGCAACGCG 1620
Db 1682 CTGCAGTACTGAAACGGGAGTACGAGGTGGAGCGCGGTGGCGGAGCGCAACGCG 1741
Qy 1621 TACCTCAAGGAGCAGACATGAGACTTTCCTCATCTTGGCGCCAGCCAGCAACCGAAA 1680
Db 1742 TACCTCAAGGAGCAGACATGAGACTTTCCTCATCTTGGGAGCCAGCCAGCAACCGAAA 1801
Qy 1681 GAGGAGAGGCCATGTGCGCAAGCTGACGCGGACTCGGGCCAACTCCATGGAAGGGCTG 1740
Db 1802 GAGGAGAGGCCATGTGCGCAAGCTGACGCGGAGCGCGGCACTCCATGGAAGGGCTG 1861
Qy 1741 ATGCCCGCTGGGTCTCTGATGTGCTTCTCCCGAGACCAAGGACTCCAAAGGCTTCCGC 1800
Db 1862 ATGCCAGCTGGGTGGCGCGGCTTCTTCCGAGCCAGGACTCCAAAGGCTTCCGC 1921
Qy 1801 CAGATGGGCATGATGATTTCCAGCAAGACAAACCGGGGCCCAAGATGCCCTGAACCCCT 1860
Db 1922 CAGATGGGCATGATGATTTCCAGCAAGACAAACCGGGGGTCCCAAGATGCCCTGAACCCCT 1981
Qy 1861 GAGGATGAGGTGATGATTTCTGAGCGCTGCATCGATCGATCGCGGAGCATTTGATCAGCTG 1920
Db 1982 GAGGATGAGGTGATGATTTCTTGGGCCCTGGGATCGATGCGCGGAGCATTCGATCAGCTA 2041
Qy 1921 CGGAAGGACATGTGCGCGCTTCTGCTCACTTCCAGAGAGAGATCTTGAAGAAG 1980
Db 2042 CGGAAGGACATGTGCGCGCTTCTGCTCACTTCCAGAGAGAGATCTTGAAGAAG 2101
Qy 1981 TACTCCGGAAGGTGATCCCGCTTTCGAGGCTACGTTGCGCTGCTGCTGTTGCTTC 2040
Db 2102 TACTCCGGAAGGTGATCCCGCTTTCGAGGCTACGTTGCGCTGCTGCTGTTGCTTC 2161
Qy 2041 TGCCTTCATCTGCTTTCATCCAGCTTCTCATCTTCCCACTCCACCTGATGCTTGGGATC 2100
Db 2162 TGCCTTCATCTGCTTTCATCCAGCTTCTCATCTTCCCACTCCACCTGATGCTTGGGATC 2221
Qy 2101 TATGCCAGCATCTTCTGCTGCTGCTAAATCAACGCTGCTCATCTGCTGCTGCTGCTGCT 2160
Db 2222 TACGCCAGTATCTTGTGCTGTTGTGATCAACGCTGCTGCTGCTGCTGCTGCTGCTGCT 2281
Qy 2161 GGTTCCTGTTCCCTAAGGCCCTTGCAACGCTGTGTCTCCGAGCATTTGCTCGCTCACGGGCA 2220
Db 2282 GGTTCCTGTTCCCTAAGGCCCTTGCAACGCTTTTCCGAGCATCGCTCGCTCTCGGGCA 2341
Qy 2221 CATAGCACCGCAGTTGGCATCTTTCCGCTGCTGCTGTTGTTACTTCTGCGCATTCGCAAC 2280
Db 2342 CACAGCATGTGGTGGCATTTTTCAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2401
Qy 2281 ATGTTTCACTGTAACACACACCCCATACGAGCTGTGCGAGCCCGGATGCTGAATTTAACA 2340
Db 2402 ATGTTTCACTGTAACACACACCCCATACGAGCTGTGCGAGCCCGGATGCTGAATTTAACA 2461
Qy 2341 CTTGCTGACATCACTGCTGCGCACTTCGAGCAGCTCAATTTACTCTCTGCGGCTGGAATGCT 2400

Db 2462 CCCGCTGACATCACTGCTGCCACCTGCGACGAGCTCAATTACTCTCTGGGCTCGATGCT 2521
Qy 2401 CCCCTGTGTGAGGGCACCACATGCCACCTGCGAGCTTCTCTGAGTACTTTCATCGGGAACATG 2460
Db 2522 CGCGTGTGTGAGGGCACCACCCACCTTGCAGCTTCCCTGAGTACTTCTGTTGGGAACATG 2581
Qy 2461 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGCGACATCAGCAGCATCGGGAAGTTGGCC 2520
Db 2582 CTGCTGAGTCTCTTGGCCAGCTCTGTCTTCTGCGACATCAGTAGCATCGGGAAGTTGGCC 2641
Qy 2521 ATGATCTTTGCTTGGGCTCATCTATTATTTGCTGCTTCTGCTGGTCCCGCCAGCCACC 2580
Db 2642 ATGATCTTTGCTTGGGCTCATCTATTATTTGCTGCTTCTGCTGGGCCCCCGCCAGCCACC 2701
Qy 2581 ATCTTTGACAACTATGACCTACTGCTTGGCGTCCATGGCTTCTTCCAAATGAGACC 2640
Db 2702 ATCTTTGACAACTATGACCTACTGCTTGGTGTCCATGGCTTCTTCCAAATGAGACC 2761
Qy 2641 TTTGATGGCTGAGCTGTCAGCTGCGAGGAGGTGGCCCTCAATATATATGACCCCTGTG 2700
Db 2762 TTTGATGGCTGAGCTGTCAGCTGCGGAGGAGGTGGCACTGAATATACATGACCCCTGTG 2821
Qy 2701 ATTCTGCTGCTTTGCTGGCTGCTGCTGCTATCTGCACTGCTCAGCAGGTGGAGTCCAGTCC 2760
Db 2822 ATTCTGCTGCTTTGCTGGCTGCTGCTATCTGCACTGCTGCTGCTGCTGCTGCTGCTGCT 2881
Qy 2761 CGCTAGACTTCTCTCGGAACTACAGGCAACAGGGGAGAGGAGAGATGAGGAGCTA 2820
Db 2882 CGCTGAGACTTCTCTGGAACCTGAGGCAACAGGGGAGAGGAGAGATGAGGAGCTC 2941
Qy 2821 CAGGCAATACACCGAGGCTGCTGATTAACATTTGCCCCAAGGAGCTGGCGGCCCACTTC 2880
Db 2942 CAGGCTTACACCGAGGCTGCTGATTAACATTTGCCCCAAGGAGCTGGCGGCCCACTTC 3001
Qy 2881 CTGGCCCGGAGCGCGCAATGATCACTCTACTATCATGCTGCTGCTGCTGCTGCTGCT 2940
Db 3002 CTGGCCCGGAGCGCGCAATGATGAGCTCTACTACCACTGCTGCTGCTGCTGCTGCTGCT 3061
Qy 2941 ATGTTTGCTTCCATTCGCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAAACAATGAG 3000
Db 3062 ATGTTTGCTTCCATTCGCAACTTCTCTGAGTTCTATGTGGAGCTGGAGGCAAAACAATGAG 3121
Qy 3001 GGTGTGAGTGTCTCGGCTGCTCAACGAGATCATCGTGTGATTTGATGAGATTAATCAGC 3060
Db 3122 GGTGTGAGTGTCTCGGCTGCTCAACGAAATCATCGCGCACTTTGATGAGATCATCAGC 3181
Qy 3061 GAGGAGCGTTCCGCGAGCTGGAAGATCAAGAGATTTGTAGCACCTACATGCTGCTGCC 3120
Db 3182 GAGGAGCGTTCCGCGAGCTGGAAGATCAAGAGATTTGTAGCACCTACATGCTGCTGCC 3241
Qy 3121 TCAGGGCTGAAGCCAGCACTTACGATCAGGTGGGCGCTCCACATCACTGCTGCTGCT 3180
Db 3242 TCAGGGCTGAAGCCAGCACTTACGATCAGGTGGGCGCTCCACATCACTGCTGCTGCT 3301
Qy 3181 GACTAGCCATGCGCTCATGAGCAGATGAAGCAATCAATGAGCATCTCTTCAACAT 3240
Db 3302 GACTATGCTATGCGCTCATGAGCAGATGAAGCAATCAATGAGCATCTCTTCAACAT 3361
Qy 3241 TTCCAGATGAAGATTGGCTGACATGAGCCCGAGTGGGAGGTGTATCGGGCTCGG 3300
Db 3362 TTCCAGATGAAGATTGGCTGACATGAGCCCGAGTGGGAGGTGTATCGGGCTCGG 3421
Qy 3301 AAGCCACAGTATGACATCTGGGGGAACAGTGAATGTCTCTAGTGTGATGAGCAGCAG 3360
Db 3422 AAGCCACAGTATGACATCTGGGGGAACAGTGAATGTCTCTAGTGTGATGAGCAGCAG 3481
Qy 3361 GGGGTTCCCGACCGAATCCAGGTGACCGGACTTGTACCGAGTTCTAGCTGCCAAGGCG 3420
Db 3482 GGGGTTCCCGACCGAATCCAGGTGACCGGACTTGTACCGAGTTCTAGCTGCCAAGGCG 3541
Qy 3421 TACAGCTGAGTGTGAGGGGTGTCAAGGTGAAGGGGCAAGGGGAGATGACCACTTAC 3480
Db 3542 TACAGCTGAGTGTGAGGGGTGTCAAGGTGAAGGGGCAAGGGGAGATGACCACTTAC 3601

Qy 3481 TTCCTCAATGGGGCCCCCAGCAGTTAAACAGGGCCCCAGCCAAATTCAGCTGAAGGGACC 3540
Db 3602 TTCCTCAATGGGGCCCCCAGCAGTTAGCAGAGCCAGCTACAAGTTCAGCTGTGAGGACC 3661
Qy 3541 AAGGTGGGCACT 3552
Db 3662 AAGGTGGGCACT 3673

RESULT 4

US-08-240-357-1
; Sequence 1, Application US/08240357
; Patent No. 5578481
; GENERAL INFORMATION:
; APPLICANT: Ishikawa, Yoshihiro
; TITLE OF INVENTION: Cloning and Characterization of a
; TITLE OF INVENTION: Cardiac Adenylyl Cyclase
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,357
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 31,705-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4046 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 131..3625
US-08-240-357-1

Query Match 85.9%; Score 3051.2; DB 1; Length 4046;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 3260; Conservative 0; Mismatches 283; Indels 9; Gaps 3;

Qy 1 ATGTCATGTTTGTAGTGGCTCTGCTCCCTAAAGTGAACGGAACACAGCTTGGGT 60
Db 131 ATGTCGTTGTTTGTAGTGGCTCTGCTCCCTAAAGTGAACGGAACACAGCTTGGGT 190
Qy 61 GAACGCAATGGGAGAGCGTTCCGGCGCGTGGCACTCGGGCAGGTGGCTTCTGCAAG 120
Db 191 GAACGCAATGGGAGAGCGT---CCAGCCCGCGGACTCGGACCAAGTGGCTTCTGCAAG 247
Qy 121 CCCCGCTATATGAGTGCCTCCCGGATGCAAGCCACCCAGCCCCACCCCTGCGGGCCCC 180
Db 248 CCCCGCTATATGAGTGCCTCCCGGATGCGCAGCCCCCAGTCCACCCCTGCGGCTCCC 307
Qy 181 CCTCGGTCCCTCGGAGGATGAGCCCTTATCCGAGGGCGGCGCCCAAGGCAAGGCAAG 240
Db 308 CCTCGGTCCCTCGGAGGATGAGCCCTTATCCGAGAGAGCGGCGCCCAAGGCAAGGCAAG 367

241 GAGCTGGGGCTGCGGGCAGGTGGCCCTTGGGCTTCGAGGATACCGAGGTGAACAACGACAGCG 300
Db |||||
368 GAGCTGGGGCTGCGGGCGGTGGCCCTTGGGCTTCGAGGACACTGAGG---CCATGTGACGG 424
Qy |||||
301 GCGGGAGCGGTGAGGTGGCGGCCCGAGACGGGTGGCCAGAGTGGGCGCATCTGCTGGCGC 360
Db |||||
425 GTTGGGGCAGCTGAGGTGGCGCCCTGAGCTGACCCCGGGAGTAGGCGCATCTGCTGGCGC 484
Qy |||||
361 CGTCTGTGAGGTGTTCCAGTCCAGACAGTTCGGTTCGGCCAGCTGGAGCGCCGTGAC 420
Db |||||
485 CGTCTGGCCAGGTGTTCCAGTCCAGACAGTTCGGTTCGGCCAGCTGGAGCGCCGTGAC 544
Qy |||||
421 CAGCGGTACTTCTCCAGATGAACACAGAGACGCTGACGCTGCTGATGGCGGTGCTGGTG 480
Db |||||
545 CAGCGGTACTTCTTCAGATGAACACAGAGCAGCTGACGCTGCTGATGGCGGTGCTGGTG 604
Qy |||||
481 CTGCTCAAGCGGTGCTGCTGGCTTTTCCAGCGCCGACCCCGCCGCTTCAGCCCTGCTAT 540
Db |||||
605 CTGCTGAAGCGGTGCTGCTAGCCCTTCATGCTGACCTGCCCCGCTCAGCCCTGCTAC 664
Qy |||||
541 GTGCACTGTGGGCTGCGCGCGCCCTGTTGCTGGGCTCATGGGTGTGTAAACGG 600
Db |||||
665 GTGGCCCTGTGGGCTGTGGCGCACCCCTCTTCGTGGCGCTCATGGGTGTGTAAACGG 724
Qy |||||
601 CATAGCTTCCGCCAGGACTCCATGTGGGTGTGAGTTACGTGGTGTGGGCATCCTGGCG 660
Db |||||
725 CACAGCTTTCGCCAGGACTCCATGTGGGTGTGAGTACGTGGTGTGGGCATCCTGGCA 784
Qy |||||
661 GCAGTGAGGTGCGGGGCGCTCTCGAGAGACCCCGCGAGCCCTCTGCGGGGCTCTGG 720
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RESULT 5
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; Sequence 11, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/726,214
; APPLICATION NUMBER: 435
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,498
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:450
; TELECOMMUNICATION INFORMATION:
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; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4131 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-726-214-11
Query Match 79.1%; Score 2810.4; DB 3; Length 4131;
Best Local Similarity 87.5%; Pred. No. 0;
Matches 3110; Conservative 0; Mismatches 436; Indels 8; Gaps 3;
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QY 3481 TTCTCTCAATGGGGGCGCCAGCAGTTTAAACAGGGCCCA--GCCACAATTTCACTGAGGGA 3538
DB |||||
QY 3530 TTCTCTCAATGGGGGCGCCAGCAGTTTAAACAGGGGCGCAGAGTGGAAATTTCAACCAAGGGA 3589
DB |||||
QY 3539 CCAAGGTGGGCACT 3552

Db 3590 CCAAGGTGGGCACT 3603

RESULT 6

US-09-008-097-3
; Sequence 3, Application US/0908097
; Patent No. 6306830
; GENERAL INFORMATION:
; APPLICANT: Hammond, H. Kirk
; APPLICANT: Insel, Paul A.
; APPLICANT: Ping, Peipei
; APPLICANT: Post, Steven R.
; APPLICANT: Gao, Meihua
; TITLE OF INVENTION: GENE THERAPY FOR CONGESTIVE
; TITLE OF INVENTION: HEART FAILURE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASCTEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,097
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dylan, Tyler M
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 22000-20567.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1812 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1812
; OTHER INFORMATION:
US-09-008-097-3

Query Match 49.6%; Score 1763.4; DB 4; Length 1812;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1789; Conservative 0; Mismatches 21; Indels 3; Gaps 1;
QY 636 TTACGTGTGTCTGGGCGCATCTCTGGGCGCAGTGCAGGTCCGGGGCGCTCTCGCAGCAGACCC 695
DB 3 TAACTGGTGTCTGGGCGCATCTCTGGGCGCAGTGCAGGTCCGGGGCGCTTTCCGAGCAGACCC 62
QY 696 GCGCAGCCCTCTCTGGGCGCTCTGGTGCCTGTGTCTTTCTGTCTACATCGCCTACACGCT 755
DB 63 GCGCAGCCCTCTCTGGGCGCTCTGGTGCCTGTGTCTTTCTGTCTATACATCGCATAACGCT 122
QY 756 CCTCCCATCCGATCGGGCTGCGCTCTCAGGGGCTGCGCTCTCCACCTTGCATTT 815
DB 123 CCTCCCATCCGATCGGGCTGCGCTCTCAGGGGCTGCGCTCTCCACCTTGCATTT 182
QY 816 GATCTTGGCCTGGCAACTTAACTTACCGTGTGTGATGCTCTCTCTGGAAGCAGCTCGGTGCCAA 875


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Db 183 |GATCTTGGCGTGGCAACTTAACCGTGGTGATGCTTCTCTGGAAGCAGCTCGGTGCCAA 242
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Db 243 |TGTGCTGCTGTTCTCTGCAACCAACGTCATTAGCATCTGCACACATATCCACAGAGGT 302
Qy 936 |GTCTCAGCGCAGCGCTTTTCAGAGAGCCCGCGGTTATACATCCAGCCCGGCTCCACCTGCA 995
Db 303 |GTCTCAGCGCAGCGCTTTTCAGAGAGCCCGCGGTTATACATCCAGCCCGGCTCCACCTGCA 362
Qy 996 |GCATGGAATCGGACAGAGCGGCTGCTGCTGTGCGTATTCGCCAGCAGCTTGCCAT 1055
Db 363 |GCATGGAATCGGACAGAGCGGCTGCTGCTGTGCGTATTCGCCAGCAGCTTGCCAT 422
Qy 1056 |GGAGATGAAGAAGACATCAACACAAAAGAGACATGATCTCCACAGATCTACAT 1115
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Qy 1116 |ACAGAAGCATGACAAATGTGAGCATCTCTGTTTGAGACATTTGAGGCTTACACAGCTGGC 1175
Db 480 |ACAGAAGCATGACAAATGTGAGCATCTCTGTTTGAGACATTTGAGGCTTACACAGCTGGC 539
Qy 1176 |ATCCAGTGCACCTCGCAGAGCTGGTCAATGACCTGAATGAGCTCTTTGCCCGGTTGA 1235
Db 540 |ATCCAGTGCACCTCGCAGAGCTGGTCAATGACCTGAATGAGCTCTTTGCCCGGTTGA 599
Qy 1236 |CAAGCTGGCTGGGAGATCACTGCTGAGGATCAAGATCTTGGGGAGCTTTACTACTG 1295
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Db 660 |TGTGTGAGGGCTGCGGAGGCCCGGGCCGACATGCCCACCTGCTGTGTGAGATGGGGGT 719
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Db 720 |AGACATGATTGAGGCCATCTCGCTGCTGAGTGTGAGGAGTGTGAATGTGAACATGCG 779
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Db 840 |CGATGTGTGTGTCATGATGTGACCTCGGCAACCAACATGAGGAGGAGCGGGCTGG 899
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Qy 1596 |AGGCGGTGGTGGGAGCGCAACCGGTACCTCAAGGAGCAGACATTTGAGACTTCTCAT 1655
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Qy 1656 |CTGGGGCCGAGCAGCAAAACGGAAGAGGAGAGGCGCATCTGCGCAAGCTGCGAGCGGAC 1715
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Db 1080 |TCGGGGCAACTCCATGGAAGGGCTGATGCGCGGCTGGGTTCTGATGCTGCTTCTCCCG 1139
Qy 1776 |GACCAAGGACTCCAGGCTTCCGACAGATGGGATGATGATTCAGCAAGACACCG 1835
Db 1140 |GACCAAGGACTCCAGGCTTCCGACAGATGGGATGATGATTCAGCAAGACACCG 1199
Qy 1836 |GGGCAACCAAGATGCCCTGAACTGAGGATGAGTGTGATGATGATTCAGCAAGACACCG 1895
Db 1200 |GGGCAACCAAGATGCCCTGAACTGAGGATGAGTGTGATGATGATTCAGCAAGACACCG 1259
Qy 1896 |CGATGCCCGCAGCATGATCAGCTGCGGAAGGACCAATGTCGCGCGGTTCTGCTCACTTT 1955
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Db 1260 |CGATGCCCGCAGCATTTGATCAGCTGCGGAAGGACCAATGTGCGCGGTTTTTGTCTACCTT 1319
Qy 1956 |CCAGAGAGAGGATCTTTGAGAAGAGTACTCCCGGAAGGTGGATCCCGGCTTTCGAGGCTA 2015
Db 1320 |CCAGAGAGAGGATTTTGAAGAAGTACTCCCGGAAGGTGGATCCCGGCTTTCGAGGCTA 1379
Qy 2016 |CGTGTGCTGTGCGCTGTTGCTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT 2075
Db 1380 |CGTGTGCTGTGCGCTGTTGCTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT 1439
Qy 2076 |ACACTCCACCTGATGCTTGGGATCTATGCGAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 2135
Db 1440 |ACACTCCACCTGATGCTTGGGATTTATGCGAGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1499
Qy 2136 |GCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2195
Db 1500 |GCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1559
Qy 2196 |CCGAGCATTTGCTCGCTCAACGGGACATAGCACCGGAGTTGGCATCTTTTCGCTGCTGCT 2255
Db 1560 |CCGAGCATTTGCTCGCTCAACGGGACATAGCACCGGAGTTGGCATCTTTTCGCTGCTGCT 1619
Qy 2256 |TGTGTTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2315
Db 1620 |TGTGTTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1679
Qy 2316 |TGCGAGCCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGACCATGCTGCGAGCTG 2375
Db 1680 |TGCGAGCCCGGATGCTGAATTTAAACCTGCTGACATCACTGCTGACCATGCTGCGAGCT 1739
Qy 2376 |CAATTAATCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2435
Db 1740 |CAATTAATCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1799
Qy 2436 |TCTGAGTACTTC 2448
Db 1800 |TCTGAGTACTTC 1812
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RESULT 7

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US-09-473-716-1
; Sequence 1, Application US/09473716
; Patent No. 6436672
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, James
; APPLICANT: Cor Therapeutics, Inc.
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
; FILE REFERENCE: 44481-5027-01-US
; CURRENT APPLICATION NUMBER: US/09/473,716
; CURRENT FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/US98/13540
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/070,901
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 08/886,362
; PRIOR FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4523
; TYPE: DNA
; ORGANISM: human type V adenylyl cyclase
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (139)..(3921)
US-09-473-716-1
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Query Match 49.6%; Score 1761; DB 4; Length 4523;
Best Local Similarity 72.2%; Pred. No. 0;
Matches 2385; Conservative 0; Mismatches 885; Indels 33; Gaps 6;
Qy 214 CGAGGGGGCGGCCCGCCAGGCAAGGAGAGCTGGGGCTGCGGCGAGTGGCCCTTGGGCTTC 273
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QY 645 GCTGGGATCTCTGGGGAGTGCAGGTGCGGGGCGCTCTCGCAGCAGACCCCGCAGGCC 704
Db 428 CATTCAGTGTGCTGGCGCTCCAGGTAGTGGCCCTGTTCCTGACACAGCCACCGCAGCGC 487
QY 705 CTCGCGGCGCTCTGGTCCCTGCTGTTCTTCTGCTACATCGGCTACACGCTCTCCGCCAT 764
Db 488 CTCGAGGGCATCTGGTGACCGTGTCTTCTATCATCATCTACACCTCTGCTGCTGT 547
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Db 1268 GTCTAACGATGTCACTGTGCCAACACATGAGACTGGCGGCAAGGCGGCGCATCCA 1327
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QY 1833 CCGGGGACCCCAAGATGCCCTGAAACCTTGAGGATGAGGTGATGATGTTCTGAGCGGTGC 1892
Db 1622 CAAGAAATGCCAGGAAGTGCACACCTTGAGGATGAAGTGAAGAGTTCCTGGGTCGAGC 1681
QY 1893 CATGATGCCCGCAGCATTTGATCAGCTGCGGAAAGCAACATGTCGCCCGTTCCTGCTCAC 1952
Db 1682 CATGATGCCAGGAGTATTGACAGACTCGGATCCGAAACGTCGCGGAAAGTTCCTCTTGAC 1741
QY 1953 CTTCCAGAGAGAGATCTTGAGAGAGAGTACTCCCGGAGGTGGATCCCGTTCGGAGC 2012
Db 1742 CTTTAGGAGCGCCGACTTAGAGAGAGAGTACTCAAGCAGGTGGATGACCGATTTGGTGC 1801
QY 2013 CTAGTTCCTGTGCTGCTGTTGGTCTTCTGCTTCTATCTGCTTTCATCCAGCTTCTCATCTT 2072
Db 1802 CTATGTGGCTGTGCTGCTGCTGTTTCTCTTCTTCTTCTGCTTTCAGATCACCATTGT 1861
QY 2073 CCCACATCCACCTGATGCTTGGATCTATGCGCAGCATCTTCTGCTGCTGCTTAATCAC 2132
Db 1862 GCGCCACTCTCTGTTCTGCTGAGCTTCTACTGTCGTGTTTCTGCTACTTGGCCTTGT 1921
QY 2133 CGTGTGATCTGCTGTGTAATCTCTGCTGCTTCTGTTTCTGTTCCCTAAGGCGCTGCAACGCT 2192
Db 1922 GGTGTTTATCTGTGATCTAGCGCTGTGTAAGCTCTTCTCTACTCTCCCTGCGAGACT 1981
QY 2193 GTCCCGCAGCATGTCCGCTCAGCGGCACATAGCACCGCAGTTGGCATCTTTTCCGCTCT 2252
Db 1982 CTCAGGAGATGTCGATCCAAGAGAACAGACCCCTGCTGGGGTGTTCACCATCAC 2041
QY 2253 GCTTGTGTTTACTTCTGCCATTGCCAAATGTTCACTGTAAACCAACACCCCATACGAG 2312
Db 2042 CCTGCTGTTCTCTCGGCTTTTGTCAACATGTTTGTGTCGCAACTTAAGAACCTGCTGGG 2101
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QY 2373 G-----CTCAATTACTCTCTGGGCTGGATGCTCCCTGTGTGAGGACACCATGCCAC 2426
Db 2162 GTCGGCTTCACTACAGCTTGGGCGCAGCAGGCTTCTGTGGCAGCCCGCAGTCCA 2221
QY 2427 CTGAGCTTCTCTGAGTACTTTCATCGGAAACATGCTGCTGAGTCTTTCGGCCAGCTCTGT 2486
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Db 2282 GTTCTGCAGATCAGCTGATCGGAAAGCTGCTCATGCTGCGCATTCAGAGCTCATCTA 2341
QY 2547 TTTGCTGCTGCTTCTGCTGGGTCCCGCAGCACCATCTTTGCACAACTATGACTACTGCT 2606
Db 2342 ---CGTGTCTATCGTAGAGTGCCTGGGTGCACACTCTTTGACAAACGCTGACTTCTGT 2398
QY 2607 TGGGCTCCATGGCTTGGCTTCTTCAATGAGACCTTTGATGGGTGGACTGTCCAGTGC 2666
Db 2399 CACCGCAATGCCATAG---ACTTCAGCAACACGGGACCTCCAGTGCCTGAGCATGC 2455
QY 2667 AGGAGGCTGGCCCTCAAAATATATGACCCCTGTGATCTTGTGTTGTTGGCTGGCGCT 2726
Db 2456 GACCAAGTGGCGTGAAGGTGTGAGGCCCATCATCTCTGTCTTCTGCTGCTGCTCT 2515
QY 2727 GTATCTGCATCTCAGCAGGTGGAGTGCAGCTGCGCGCTAGACTTCTCTCGAAACTACA 2786
Db 2516 GTATCTGCATCTCAGCAGGTGGAAATCCACTGCTGCGCTTGCCTTCTCTGAAACTGCA 2575
QY 2787 GGCACACGGGAGAGGAGGAGTGGAGGACTACAGGCATACAAACCGGAGGCTGCTGCA 2846

Db 2854 GACCTAGAGAGATCAAGACCATTTGGGAGCACGTACATGCTGCTGTGGGGCTGGGGCC 2913
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Db 2914 ACTGCTGGGACCAAGGCTAAGAGTGATCTCTCCACCTCAGCAGCTTGGCAGATTTT 2973
Qy 3187 GCCATGGGCTCATGGAGCAGATGAAGACATCAATGAGCACTCTTCAACAATTTCCAG 3246
Db 2974 GCCATCGAGATGTTGATGCTCTGGATGAGATCACTACAGTCTTATAACGACTTTGTG 3033
Qy 3247 ATGAAGATTCGGCTGAACATGGGCCAGTCTGTCAGGCTGTCATCGGGCTTCGGAAAGCCA 3306
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Qy 3307 CAGTATGACATCTGGGGGAACACAGTGAATGCTCTAGTCTGATGAGCAGCAGGGGGTC 3366
Db 3094 CAGTATGACATTTGGGGGAACACAGTCAATGTCAGTCCAGTGGATGGACAGTACCGGGTC 3153
Qy 3367 CCGACCGAATCCAGGTGACACGGACCTGTACCAGTTCTAGCTGCCAAGGGCTACCAG 3426
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Qy 3427 CTGAGTGTCTCAGGGGTGGTCAAGGTCAAGGGCAAGGGGGAGATGACCACTACTTCTC 3486
Db 3214 TTGCTGTGCCAGGCAAGTCAGTGTCAAGGGCAAGGGTGGATGCTGACATCTTCTG 3273
Qy 3487 AATGGGGGGCCCC 3498
Db 3274 GAAGGCAGGACC 3285

RESULT 10

US-09-412-210-2
; Sequence 2, Application US/09412210
; Patent No. 6403358
; GENERAL INFORMATION:
; APPLICANT: Kapellier-Libermann, Rosana
; TITLE OF INVENTION: 21529, A NOVEL ADENYLATE CYCLASE
; FILE REFERENCE: 5800-47
; CURRENT APPLICATION NUMBER: US/09/412,210
; CURRENT FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 3518
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: 21529 adenylate cyclase
; NAME/KEY: CDS
; LOCATION: (247)...(3480)
US-09-412-210-2

Query Match 14.48; Score 512.4; DB 4; Length 3518;
Best Local Similarity 49.84; Pred. No. 1.4e-114;
Matches 1571; Conservative 0; Mismatches 1506; Indels 75; Gaps 8;
Qy 409 GAGCGCCTGTACCAAGCGGTACTTCTCCAGATGAACAGAGCAGCCTGACGCTGCTGATG 468
Db 286 GACCTCTTACGAGACTTACTAGCCTGAGCCAGCAGTACCGCTGCTGCTGCTG 345
Qy 469 GCGGTGTGTGTGCTTCAAGCGGTGCTGCTGCTGCTTTCACCGCCAGCCCGCCCT 528
Db 346 CTGGGATCGTGTCTGTGGCTCGCGGCTGTCTCGAGTGGCTTGGGCGAGCGG 405
Qy 529 CAGCTCCCTATG-----TGGCACTGTGGCTGTGCGCGCGCTGCTGCTG 576
Db 406 GAGCTGACCTCAGACCCAGAGCTTCTGACCACTGTGCTGCGGCTGCGGCTTCTCG 465
Qy 577 GGGCTCATGTGTGTGTAAACCGGCATAGTCTTCGCCAGGACTCCATGTGGGTGGT 636

Db 466 CTGCTGCTGGGCTCTGCTTCCGGGAGCAGCGACTCAGCGCTGGACGGCTCCCTGTCC 525
Qy 637 TAGTGTGCTGGGCATCTGGGGCAGTGCAGGTGGGGGGCTCTCCGACGAGACCG 696
Db 526 GGTGGTATGGGTGCGCTGTAGCGCTAGGCCACGCTTCTGTGTACCGGGGGCGTG 585
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Qy 1438 GTGCACTCGGGCTCTTGGCTTTCGGAAATGSCAGTTCGATGTGTGCTCAATGATGTG 1497
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Qy 1498 ACCCTGGCCACCATGAGGAGGAGCGGGCTGGCGCATCCACATCACTCCGGCA 1557
Db 1426 ACATGGCTAAACCATGAGGAGCGGCTGTACAGGGCGAGTGCACATCACAGGGGCT 1485
Qy 1558 ACATGCACTTACCTGAACCGGGGACTACGAGGTGAGCGAGCGGCTGTGGCGAGCGCA 1617
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Db 1546 CCTACCTTCGGAGCTAGGAGCCTACCTATCTGGTCTATCGATCCAGCGGAGAGGAG 1605
Qy 1678 AAGAGGAGAGGCCATCTGGCCAAAGCTGCGAGGACTCGGGCCAACTCCATGGAAGGG 1737
Db 1606 GAGGATGAGAAGGCACTGACAGAGGCTTGCTGCTCTGCTTGAGGGCTCAAGATGCGT 1665
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Db 1666 CCATCACTGCTGATGACCGGTTTACCTGGAGTCTCTGGGGGACGCAAGGCTTTTGGCCAC 1725
Qy 1798 CGCCAGATGGGATGATGATGATTCAGCAAGAACACCGGGGACCAAGATGCCCTG--A 1855
Db 1726 CTGAGCCAGGAGACAGCCCTGTGTCCACTCAACCCCTCTCCGGAGAGACCTTGGCT 1785
Qy 1856 ACCCTGAGATGAGTGA--TGAGTTCTGAGCCGTGCGATCGATGCGCGCAGCATTTGAT 1914
Db 1786 TCCTTCAGCACCCAGTGGAGCTGGATCGAGCGGTACCCCGGGGACTAGATGATGNA 1845
Qy 1915 GAGCTGCGGAAGACATGTGGCCGGTTTCTGCTCACCTTCCAGAGAGAGGATCTTGAG 1974
Db 1846 CTGGACACCGGGGATGCCAAGTTCTTCCAGGTCATTGAGCAGCTCAACTCGCAGAAACAG 1905
Qy 1975 AAGAGTACTCCCGGAAGTGGATCCCGCTTCGGAGCCTACGTTGCGCTGTCCTGTTG 2034
Db 1906 TGAAGCAGTGAAGACTTCAACCACTGACACTGTACTTCAGAGAGAGGATGGAG 1965
Qy 2035 GTCTTCTGCTTCATCTGCTTCATCCAGCTTCTCATCTTCCACACTCCACCTGATGTT 2094
Db 1966 AAGAGTACCGACTCTCTGCAATCCCGCTTCAAATATATATGAGCCTGCACCTTCCTG 2025
Qy 2095 GGGATCTATGCCAGATCTTCTGCTGCTGCTTAATCACCGTCTGATCTGTGTGTGATC 2154
Db 2026 GTTTTCTCTCAACTTCATCATCCAGATGCTAGTGACAAACAGAGCCCGCCAGCTCTGGCC 2085
Qy 2155 TCCTGTGTTCTCTGTCTTAAGCCCTGCAAGCTCTGTCCGGCAGCATTTGTCGCTCA 2214
Db 2086 ATCAC---GTAAGATCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 2142
Qy 2215 CGGGCACATPAGCACCGCAGTGGCATCTTTCCGCTCTGTTGTTGTTACTTCTGCCATT 2274
Db 2143 GAGGACCTGATGAGTGTGTCTGAAAGGCCCCAGAGTGTGCTGCTGCTGCTGCTGCTG 2202
Qy 2275 GCAACATGTTCACTGTAAACACACCCCATACGGAGCTGTGACGCGGAGTGTGTAAT 2334
Db 2203 TCTGGCTGTGGGACACAGCAGCAGGACTGAGAATAGCTTGGGACCGCCACCATCTCTC 2262
Qy 2335 TTAACACCTGCTGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2394
Db 2263 CTGTGCTTGGCATGGCCATTAACAGCCTGTTCTTCTTCCCAACATCATCAGACTGCCCT 2322
Qy 2395 GATGCTCCCTCTGTGAGGGACCATGCCACCTGCGAGCTTCTCTGAGTACTTTCATCGGG 2454
Db 2323 TTCCAAAGCTCCCAATGTGCTCCATGATTTCCAACTCTCTGAGAGCTCTCTGGGTCT 2382
Qy 2455 AACATGCTGCTGAGTCTCTTGGCCAGCTGTGCTTCTGCAATCAGCAGCATCGGGAAG 2514
Db 2383 CTGCTCTCATCAGTGTCCCATCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2442
Qy 2515 TTGGCCATGATCTTGTCTTGGGCTCATCTATTTGGTGTCTCTCTGCTGCTGCTGCTGCTG 2574
Db 2443 TCCCTCTTCTGCAATGAGCTTTCAGCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2502
Qy 2575 GCCACATCTTTGACAACTATGACCTACTGCTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2634
Db 2503 GCATCTGCTCCTCTTCTGCTGCTCCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2562
Qy 2635 GAGACCTTTGATGGGCTGAGTGTCCAGTGTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2694
Db 2563 CTCTATCTGGGCCCCCTGAGCTCCAGGCGCGAGTGTGCTGAGAGGCCCAAACTGATGGT 2622
Qy 2695 CTTGTGATCTGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2754
Db 2623 GCTATCT 2682

Qy 2755 ACTGCCCGCTAGACTTCTCTGGAACCTACAGGCAACAGGGGAGAGGAGGATGGAG 2814
Db 2683 TACTGCCCGCTGAGCTTCTCTGGAAGAAGAGCTGAGGAGGAGGAGGAGACAGAG 2742
Qy 2815 GAGCTACAGGATACAAACCGGAGGCTGCTGATTAACATCTTCTGCCCAAGGAGCTGCGGCGC 2874
Db 2743 ACATGAGGAAACCTGACTCGGCTGCTCTTGAGAAACGCTCTCCCTGCACACGCTGGCCCC 2802
Qy 2875 CACTTCTTGGCCCGGAGCGCGCAATGATGAACCTCTACTATCACTGCTGCTGAGTGTG 2934
Db 2803 CAGTTCTTGGCCAGAACCGGCGCAACGAGGATCTCTACCACTGCTCTATGAATGCGTT 2862
Qy 2935 GCTGTATGTTTGGCTTCCATTGCCAATCTTCTCTGAGTTCTATGTGGAGCTGAGGCAAAAC 2994
Db 2863 TGTGTCTTCTTGGCTTCCAGTCTTCCAGCTTCAAGGAGTTCTACTCTGATCCAAACATCAAT 2922
Qy 2995 AATGAGGCTGTGAGTGTGCTGCGGCTGCTCAACGAGATCATCGCTGATCTTTGATGAGATT 3054
Db 2923 CATGAGGCTTAGAGTGTCTGAGGCTGCTCAATGAGATAATTTGCTGATTTTGTGAGCTG 2982
Qy 3055 ATCAGCGAGGAGCGGTTCCGCGAGCTGGAAGATCAAGACGATTTGGTAGCACCTACATG 3114
Db 2983 CTCTCAAGCCCAAGTTCAAGTGGGAGGAGATCAAGACCATCGGAGCAGCCTACATG 3042
Qy 3115 GCTGCTCAGGCTGAACCGCAGCAC-----CTACGATCAGGTGGGC 3156
Db 3043 GCAGCCACAGGCTTAAATGCCACCTCTGGACAGGATGCACAACAGGATGCTGAACGGAGC 3102
Qy 3157 CGCTCCACATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3216
Db 3103 TGCAGCCACCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3162
Qy 3217 ATCAATGAGCACTCTTCAACAATTTCCAGATGAAGTTGGGCTGCAATGGGCCCCAGTC 3276
Db 3163 ATCAAGAGCAATCATTCACAACCTTCCGCTGCGAGTGGGTTGAACCATGGACCCGTA 3222
Qy 3277 GTGCAGGCTGTCTGCGGCTCGGAAGCCACAGTATGACATCTGGGGGAAACACAGTGAAT 3336
Db 3223 GTAGCTGAGTTATTTGGGCCCCAGAGCCGCAATATGACATTTGGGGGCAACACAGTGAAC 3282
Qy 3337 GTCTCTAGTCTATGAGACGACCGGGGTCGCCAATCCGAAATCCAGGTGACACCGACCTG 3396
Db 3283 GTGGCCAGCCCATGAGAGTACAGGAGTCTTGGCAAAATCCAAGTCACTGAGGAGACA 3342
Qy 3397 TACCAGTTCTAGCTGCCAAGGCTACAGCTGAGTGTCCAGGGGTGCTCAAGGTGAAG 3456
Db 3343 GCATGGGCCCCCTACAGTCCCTGGGCTACACCTGCTACAGCCGGGTGTCTCAAGGTGAAG 3402
Qy 3457 GGCAAGGGGAGATGACCACTTCTCTCAA 3488
Db 3403 GGCAAGGGGAGCTCTGCACCTACTTCTGNA 3434

RESULT 11

US-08-726-214-15
; Sequence 15, Application US/08726214
; Patent No. 6107076
; GENERAL INFORMATION:
; APPLICANT: Tang, Wei-Jen
; APPLICANT: Gilman, Alfred G.
; TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYL CYCLASE
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726.214
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/005,498
; FILING DATE: 04-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UTSD:450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-726-214-15

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Qy	1363	ATTGAGGCCAATCTCGCTGGTACTGTGAGGTGACAGGTGTGTAATGTGAACATGCGCGTGGGC	1422
Db	2235	ATCAAAACTATCAGGTTTGTGAGGTCAGAAACGAAGCATGATCTGCATATCGAAATTGGA	2294
Qy	1423	ATCCACAGCGGCGGTGCACCTGGGCGTCTTGGCTTGGGAAATGGCAGTTTCGATGTG	1482
Db	2295	ATCCATTTCAGGCTCTGTGCTGTGTGTGTGTGGGCTGAGAAATATGGCAGTTTGTATGTC	2354
Qy	1483	TGTTCCAAATGATGTACCCCTGGCCAAACCATATGGAGCGAGAGCGCGGCTGCCGCATC	1542
Db	2355	TGTTCTTGGAGTGTGNCATCGCAACAACTTGAATCTGGAGAGATCCCTGGAGAAATT	2414
Qy	1543	CACATCACTCGGGCAACACTGCACTGAGTACCTGAAACGGGGACTACGAGGTGGAGCCAGCCGT	1602
Db	2415	CACATTTCCAAAGCCACACTGGATTGCTCAGTGGTGACTATATAATGTGGAAGAGGSCCAC	2474
Qy	1603	GTTGGCGAGCGCAACGGTACCTCAAGGAGCAGACATTTGAGACTTTCTCATCTCTGGGC	1662
Db	2475	GGTAAGGAGAGGAATGAATTTCTTGGAGAGCATATAATAGAGACCTATTTTGATTAAGCAG	2534
Qy	1663	GCCAGCCAG-----AAACCGAAAGAGGAGAAGGCCATCTCTGGCCA	1702
Db	2535	CCCGAGAGAGTTTGCTATCTTCCCTGGAAGATATAGTTAAGAGTCCGTGAGACTGCTCG	2594
Qy	1703	AGTGTACAGCGGACTCGGGCCAACTCCATGGAAGGGGTGATGCCGCGCTGGTTCTCTGATC	1762
Db	2595	GACAGGAGAAACAGTGGGGCAAGGTTTACAGAAAGGATCTTGGAGCCAGAACTGCCATTCT	2654
Qy	1763	GTGCCTTCTCCGGACCAAGGACTCCNAGGCTTCCGCCAGATGGGCATTTGATGATTC--	1820
Db	2655	GACAACATCTGTGGGCAACAGAAATCTCTGGCTGCCCTAACAGAAATTTCAATTAATCTGT	2714
Qy	1821	--CAGCAAAAGACAACCGGGCACCAAGATGCCCTGAAACCCCTGAGGATGAGGTGGATGAG	1878
Db	2715	CTTCCAAACCATCTCGCAACAAGCTTTTGATGTCCAGTCTGGGCTCAGGNAATTAACAAG	2774
Qy	1879	TTCTGTAGCGCTGCCATTCGATGCCCGACGATTTGATCAGCTCGGAGGACCAATGTGCGC	1938
Db	2775	AGAATAGAGCATACCATCGACTTTCGGAGTGGCGATAAGTTGAGAAGAGAGCATATCAAG	2834
Qy	1939	CGGTTTCTGTCTACCTTCCAGAGAGGATCTTTGAGAGAAAGTACTCCCGAAGGTGGAT	1998
Db	2835	CCATTCTCACTGATTTTAAAGACTCCAGCTTGGAGCAACAAGTATTTCTCAAAATGCGGGAT	2894
Qy	1999	CCCGCTTTCGGAGCTACGTTGCTGTGCCCTGTGGTCTTTCTGTCTCATCTCTCTCATC	2058
Db	2895	GAAGTATTCAAGTCAAACTTGGTCTGTGCATTTATCGTTCTCTGTGTATCATCTCGGAT	2954
Qy	2059	CAGTTCTCATCTTTCCACACTCCACCCTGATGCTTTGGGATCTATGCCAGCATCTTCTCTG	2118
Db	2955	CAAAGT---TTGCTTCTCTTTCGAGGCTGATGCCATGACCATCAAGTTTCTCCATCTCTG	3011
Qy	2119	CTGCTGTCAATACCGTGTGATCTGTGCTGTGTACTCTCTGTGGTTCCTGTTCCTTAAG	2178
Db	3012	ATCATGCTGCACTCCGCGCTTGT-----CCTCA	3039
Qy	2179	GCCCTGCAACGTCTGTCCCGACGATTTGCCGTTCAGGGSCACATAGCACCGCAGTTGGC	2238
Db	3040	TCACCGGCGGAGAGACTATAAGTGTCTGCTCTCATTTCTCCGCAAAACCTGTGTGTG--	3097
Qy	2239	ATCTTTTCCGTCTGTGTGTGTTTACTTCTGCAATGTCACCAATATGTTCACTGTAAACCA	2298
Db	3098	-----GATTAAAGAGACCTATTTGGCCCGCAACGTATCATCTTTGCTTCTC	3143
Qy	2299	ACCCCATACGAGCTGTGACGCGCGGATGCTGAAATTTAACACCTGCTGACATCATCTGCC	2358
Db	3144	ATCTTGATTAATTTTCTCTGGAGCGGTCATAAAATATTCTGTGTGTGATTTTGTACAAGTCG	3203
Qy	2359	TGCCACCTGACGAGCTCAAAATTAATCTCTGGGCTGTGATGCTCCCTGTGTGAGGSCACC	2418
Db	3204	ATACCTTTGAAGAACCTTGACTTTCAAT-----TCCTCAGCTGTGT-----TT	3245
Qy	2419	ATGCCCACTGCGAGCTTTCTGTAGTACTTTTCATCGGGAACATGCTGCTGTGATCTCTTGGCC	2478

ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSD:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4008 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-726-214-3

Query Match 12.9%; Score 458.6; DB 3; Length 4008;

Best Local Similarity 50.1%; Pred. No. 1.8e-101;
Matches 1346; Conservative 0; Mismatches 1279; Indels 60; Gaps 6;

Qy	852	CCTCTGGAAGACGCTCGGTGCGCAATGCTGCTCTCTCTCCACCAAGTCATTGGCAT	911
Db	624	CCTGCTTGGGAGATGACTGGCCCAATGATCATTTTTCATTGTTGGAACTTGGCGGGAGC	683
Qy	912	CTGCACACATATCCAGCAGAGGTGCTCAGCGCCAGGCGCTTTCAGGAGACCCGCGGTTA	971
Db	684	CTACCAAGACCTCATGGAGCTTGGCTTGCAGCAAACTATCGGACACGCTGTAATTG	743
Qy	972	CATCAGGCGCGCTCCACCTGCAGCATGAGATCGGAGCAGGAGCGGCTGCTGCTGC	1031
Db	744	CATCAAGTCCCGGATCAAGCTGGAATTTGAAAAACGGCAGCAGGAACGGCTCTGCTCTC	803
Qy	1032	GGTATTGCCCGACGCTGTCATGGATGGAAGAAAGACATCA-----A	1076
Db	804	CTTGCTGCAGCTCATCTGCCTCGCATGAGATGAAAGCTGAATCATTCAGAGGCTCAGGG	863
Qy	1077	CACAAAAAAGAACATG-----ATGTTCCAAAGATCTACATACAGAAGCA	1124
Db	864	CCCCAAAGCAGCAGATGGAACACACAAACAACTTCCAGAACTGTATGTCAAACGACA	923
Qy	1125	TGACAAATGTCAGCATCTGTTGCGACATATGAGGCTTCCACAGCTGGCATCCCATG	1184
Db	924	CACCAACGTGAGCATATTATACGCTGACATGTTGGCTTACCCGCTTGCAGAGGATTG	983
Qy	1185	CACCTCGCAGGAGTGGTTCATGACCTGAATGAGCTCTTTGCGCGTTTGACAAGCTGSC	1244
Db	984	CTCCCTCGGCACTGGTGGCCATGCTGAATGAATCTTTGGGAAGTTTGATCAATAGC	1043
Qy	1245	TGCGGAGATCATCTGCTGAGGATCAAGATCTTTGGGGAGCTGTTACTACTGTGTGTCAGG	1304
Db	1044	AAAGGAGAATGAATGCATGAGAATTTAAATTTTAGGAGACTGCTATTACTGTGTTCCGG	1103
Qy	1305	GCTGCGGAGGCGCGGCGGACCATGCCACTGCTGTGTGGAGATGGGGGTAGACATAT	1364
Db	1104	GCTCCCTATATCACTCCCTTAACCATGCCAAGAACTGTGTGAAAATGGGAATGGATATGTG	1163
Qy	1365	TGAGGCCATCTCGTGGTACGTGAGTGACAGGTGGAATGGAACATCGGCTGGGCAT	1424
Db	1164	CGAAGCCATAAAGAAAGTGAGGAGTGTACCGGAGTTGATATCAACATGCGGTAGGAGT	1223
Qy	1425	CCACAGCGGCGGTGCATCGCGGCTCTTGGCTTGGGAAATGGCAGTTCGATGTGTG	1484

Db	1224	GCATTTCTGGAAACGTTCTCTGTGTGTGATTTGGTCTCCAGAAAGTGGCAGTATGATGTGTG	1283
Qy	1485	GTCCAAATGATGTGACCTCGGCGCAACCATCATGAGGACGAGGCCGGGTGCGCGCATCA	1544
Db	1284	GTCTCATGATGTTACTCTTGGCAAAACCATGGAAGCTGGAGAGTCCCTTGGCGGTGTTCA	1343
Qy	1545	CATCACTCGGGCAACACATCTGACGTACTGAAACGGGACTACGAGGTGGAGCGAGCGCGTGG	1604
Db	1344	CATTCTTTCAGTCACTCTGGAGCACTTGAATGGGCTTATAAGTTGGAGGAGAGATGG	1403
Qy	1605	TGGGAGCGCAACCGGTACTCTAAGGACGACACATGAGACTTTCCTCATCTCGGCGCG	1664
Db	1404	TGAGATAAGAGACCCCATATTTTAAAGCAGCACTTGGTGAAGAACTACTTTTGAATCAATCC	1463
Qy	1665	CA---GCCAGAAACGGAAGAGGAGGCCATGCTGGCCCAAGCTGCAGCGGACTCGGGC	1721
Db	1464	CAAGGAGAGCGACGAGTCTCTCAGACTCTCTTTCAGACTCGACACACTTGGACGGAGC	1523
Qy	1722	CAACTCCATGGAAGGGCTGATGCGCGCTGGGTTCTCTGATCGTGTGCTTCTCCCGGACCAA	1781
Db	1524	CAAGATGAGACATCTGTCCGCATGACCCGCTACTTGGAGTCTTGGGAGCAGCCAGCC	1583
Qy	1782	GGACTCCAAAGCGCTTCCGCCAGATGGGCAATTGATGATTTCCAGCAAGAACACCGGGGAC	1841
Db	1584	ATTGCGACATCTGCACCACAGAGATAGCATGACCACAGAGAATGGGAAGATTAGTACCAC	1643
Qy	1842	CCAGATGCCCTGAAACCTGAGGATGAGTGGATGAGTTCTCTGAGCGCTGCCATCGATGC	1901
Db	1644	GGATGTGCAATGGTCAACATAATTTTCAAAATGCGACCTTTAAGAACTAAGTCAAGAA	1703
Qy	1902	CGCAGCATTTGATCAGCTGCGGAAGGACCATGTGCGCGGTTTCTGTCTCACCTCCACAG	1961
Db	1704	GAGAGATTTCAGAGAGACTGATGAAGAGATGATCCAGCAATTGATGGATCAATGC	1763
Qy	1962	AGAGATCTTGAAGAAAGTACTCCCGAAGGTGGATCCCGCTTCGAGCGCTACGTTGC	2021
Db	1764	ACAGAAGCAATGGCTCAAGTCAGAAGACATTTCAAAGAACTCTCCCTGCTTTCTATAACA	1823
Qy	2022	CTGTGCCCTGTGTCT	2081
Db	1824	GAATATAGAAAGAAATACCGAGCTATGCACTGCCAGCATTTCAAGTACTACGTGACCTG	1883
Qy	2082	CACCTGATGCTGGGATCTATGCGAGCATCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	2141
Db	1884	TGCTGCTCATCTTCT	1943
Qy	2142	CTGTGCTGTGTCT	2201
Db	1944	CATCTTGGCTTCT	2003
Qy	2202	CATTGTCCGCTCAGCGGACATAGCAGCGAGTTGGCATCTTTTCCGCTCTCTCTCTCTCTCT	2261
Db	2004	CTTCGCTGGACAGCTTTTGGCAATGCGCAAAAGGCTCTCCACCTCTCTCTCTCTCTCTCT	2063
Qy	2262	TACTTCTGCCATTGCAACATGTTTCACTGTAAACACACACCCCATGAGAGCTGTGCAGC	2321
Db	2064	GAATCATCAG-----GCATCATCGCCAAACCGCCCATGGCCACGGATCTCCCTCAC	2114
Qy	2322	CCGATGCTGAATTTAAACACTGCTGACATCACTGCTGCCACCTTCGACAGCTCAATTA	2381
Db	2115	AATCGTCAACACGGCTATCATCTAAACCATGGCTGTGTTCACATGTTTTTCTCTGAGCAA	2174
Qy	2382	CTCTCTGGCGCTGGATGCTCCCTGTGTGAGGGGACCATGCGCCACTGCGAGCTTCTCTGA	2441
Db	2175	CTCTGAGGAGCAACCCCTCTCCACTGCGCAATATCAATCAAAATGCAAAACGTTTCTGTCC	2234
Qy	2442	GTACTTTCATCGGGAACATGCTGTGCTGTCTGTGCGGAGCTGTGCTCTCTCTGACATCAG	2501
Db	2235	TAAACAGCGCTGATTTCTTATGCTCGAAACCTGTGTGTCTCTCTCTCTCTCTCTCTCTCT	2294
Qy	2502	CAGCATCGGGAAGTTGGCCATGATCTTGTCTTGGGCTCATCTATTTGGTGTCTCTCTCT	2561

QY 3444 GGTCAAGGTGAAGGGCAAGGGGAGATGACACCTACTTCTCAA 3488
DB 3252 CATCAATGTGAGGGGAAGGGGACCTGAAGACATATTTTGTAAA 3296

RESULT 15

US-09-016-434-1344
; Sequence 1344, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1344:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2731 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g349268
; US-09-016-434-1344

Query Match 12.8%; Score 456.2; DB 4; Length 2731;
Best Local Similarity 52.8%; Pred. No. 5,6e-101;
Matches 1274; Conservative 0; Mismatches 1023; Indels 114; Gaps 9;

QY 1090 GACATGATGTTCCAAAGATCTACATACAGAAGCATGACAAATGTACAGATCCTGTTGCA 1149
DB 24 GAGAGGATTTTCCAAAGATTTACATCCAGAGGCACGACAAATGTGAGCATCCTGTTGCT 83
QY 1150 GACATTGAGGCTTCCACAGCTGGCATCCAGTGACTCGGAGGAGCTGGTCATGACC 1209
DB 84 GACATCGTGGGTTTTCACGGGCTTGGCATCCAGTGACAGCCAGGAGCTGGTGAACATC 143
QY 1210 CTGAATGAGCTCTTTGCGCGGTTTGACAAAGCTGGCTCGGAGATCACTGCTGAGGATC 1269
DB 144 CTCAATGAGCTCTTCGGCAAGTTCATGAATTAGCCACGAGAACCACTGTGCGCGATC 203
QY 1270 AAGATCTTGGGGAGCTGTTACTACTGTGTGTCAGGCTGCGGAGGCCCGGGCGGACCAT 1329
DB 204 AAGATCTCGGGAGCTGCTACTACTGCGTGTGCGGCGCTCACCCAGGCCCAAGACTGACCAT 263

QY 1330 GCCCACTGCTGTGTGAGATGGGGTAGACATGATTGAGGCCATCTCGCTGGTAGCTGAG 1389
DB 264 GCCCACTGCTGTGTGAGATGGGACTCGACATGATTGATACCATCACTGTGTGGCTGAA 323
QY 1390 GTGACAGGTGTGAATGTGAACATGCGCGTGGGCATCCACAGCGGGCGGTGCACTGCGGC 1449
DB 324 GCCACCGAGGTGATCTGAACATGCGGTGGGTCTGCACACCGGCGAGGTCTCTGTGGT 383
QY 1450 GTCTTGGCTTGGGAAATGGCAGTTGATGTGTGTGTCATGATGTGACCTTGGCCAC 1509
DB 384 GTCTTGGCTTGGCAAGTGGCAGTACGACGTGTGTGTCCTCAATGATGTGACCTTGGCCAAT 443
QY 1510 CACATGGAGCGAGGAGCGCGCTGCCGATCCATCACTCGGCGCAACACTGCGAGTAC 1569
DB 444 GTCATGGAAGCGCTGCGCTGCCAGGGAAGTTTATATACAAAGAGACCTTAGCGTGC 503
QY 1570 CTGAACCGGGGACTACGAGGTGGAGCGGCGGTGGTGGGAGCGCAACCGGTACTCAAG 1629
DB 504 TTGAATGGGGACTACGAGGTAGAACCGGTTACGGACATGAGAGGAACAGTTTCTTGA 563
QY 1630 GAGCAGCATTTGAGACTTTCTCTATCTTGGGGCCAGCCAGCAAGAAAGAGAGAAG 1689
DB 564 ACTATAACATCGAAACCTTTTATTGTGCCATCCCATCGCCGAAAGATATTTCCAGGC 623
QY 1690 GCCATGCTGGCCAAAGCTGCGAGGAGCTCGGGGCCAACTCCATGGAAGGGCTGATGCCGC 1749
DB 624 CTGATTCTCTCAGATATAAACCC-----GGCCAAAGGATGAAGTTCAAGACTGTCTGC 677
QY 1750 TGGGTTCTCTGATCGTGCCTTTCTCCGGGACCAAGGACTCCAAGGCTTTCCGCCAGATGGGC 1809
DB 678 TACCTGCTGTGCAGCTCATGCACTGCCGGAATAATGTTCAAGGCCGAGATCCCTTCTCC 737
QY 1810 ATTGATGATTCAGCAAGAAAGAACCCGGGCAACCCAAAGATGCCCTGAGGATGAG 1869
DB 738 AATGTCATGACCTGCGAGGACGA-----TCACAAGCGGAGGGC 775
QY 1870 GTGGATGAGTTCTCTGAGCGCTGCATCGATCCCGCAGCATTCATCAGCTGCGGAAGGAC 1929
DB 776 ATTAAGAAAGCTTCGAAAGAACTCAGAAACCGCTCATCTTTTCTTACCAAG-----828
QY 1930 CATGTGCGCGGTTTCTGCTCACTTTCCAGAGAGAGGATCTTGAGAGAGATGATCCCCG 1989
DB 829 -----TTGCTTACACCCCGGCACTCGCGTCAACAGGTACATCAGCGC 875
QY 1990 AAGTGTGATCCCGCTTCGAGGCTAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2049
DB 876 CTCTTAGAAGCCCGCCAGACAG---AGCTGGAGATGGCAGACCTGAACCTTTTACCCCTG 932
QY 2050 TGCTTCATCCAGCTTCTCATCTTCCCACTCCACCTGATGCTTGGGATCTATGCCAGC 2109
DB 933 AGTACAAACATGTCGAAACGGGAGGAAAGTACACACAGCTTCAGACAGATATTTCAAC 992
QY 2110 ATCTTCTGCTGCTGCTGAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2169
DB 993 AGCGCGTTGCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
QY 2170 TTCCCTAAGCCCTTGCAAGCTGTGCTCCGAGCATTTGTCCGCTCAGCGGCAATAGCAC 2229
DB 1053 TTCCCAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1112
QY 2230 GCAATTTGGCATCTTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2289
DB 1113 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1161
QY 2290 TGTAAACCAACCCCTATACGAGCTGTGCAAGCCCGGATGCTGAATTTAAACACCTGCTGAC 2349
DB 1162 TGACGATTCAGATTCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1221
QY 2350 ATCACTGCTGCCACCTGCGAGGAGCTCAATTAATCTCTGCGGCTGAGATGCTGCTGCTG 2409
DB 1222 CCAAGG-----TTGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1271

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QY 2410 GAGGGACCATGCCACCTGCGAGCTTCTGTAGTACTTCAATCGGGAAACAATGCTGCTGAGT 2469
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QY 2470 CTCTTGGCCAGCTCTGTCTTCTGTCGACATCAGCAGATCGGGAAGTTGGCCATGATCTTT 2529
Db 1332 TCGGAGTCTACACCATGCCCTGTCTGCTGCTGCTGGTGGGCAACCTCCCGTAGCCATA 1391
QY 2530 GTCTTGGGCTCATCTATTGAGTGTCTTCTGTGGGTCCCGCCAGCCACCATCTTTGAC 2589
Db 1392 TTTTTCGGGGTGTCTCTCTTGCCTTGCCTGCTCTCGGGCTCACACGCTCCTAC 1451
QY 2590 AACTATGACCTACTGTTGGGCTGCATGGCTTGGCTTCTTCCAATGAGACCTTTGATGGG 2649
Db 1452 ATCCTCGTTCTGAGGCTCAGCGGATACACAGGAC----- 1486
QY 2650 CTGGACTGTCCAGCTGCGAGGAGGTGGCCCTCAAAATATATGACCCCTGTGATTCTGTG 2709
Db 1487 -----TGGGGGTGGTGGCTCTCCGGGGCGAGCTACGAGCCGATTGTGGCCATCTCTG 1538
QY 2710 GTGTTTGGCGTGGCGTGTATCTGCATGCTCAGCAGGTGGAGTGCAGCTGCCCGCCTAGAC 2769
Db 1539 CTCCTTCTCTGTGGCTGGCCCTGCATGCCAGCAGGTGGACATCAGGCTGAGGCTGGAC 1598
QY 2770 TTCCTCTGGAACCTACAGGCAACAGGGAGAGAGGAGGATGGAGAGCTACAGGCATAC 2829
Db 1599 TACCTCTGGGGCCGACAGGCGAGGAGGAGCGAGAGGACATGGAGAGGTGAAGCTGGAC 1658
QY 2830 AACCGGAGGCTGCTGCATACATCTTCCCAAGGAGCGTGGCGGCCACTTCCCTGGCCCCGG 2889
Db 1659 AACAGGCGCATCCTTCAACCTCTGCGGGCCCGTCCCGCCAGCATCTTCTCATGTCC 1718
QY 2890 GAGCGCGCAATGATGAACCTCTACTATCAGTCTGTGTGAGTGTGTGCTGTTATGTTTGGC 2949
Db 1719 AACCTCGGAACATGGAACCTCTACTACGATCTTACTCCAGGTGGGGCTCATGTTTGGC 1778
QY 2950 TCCATTGCCAACTTCTCTGAGTCTATGTGGAGCTGGAGGCAAAACAATGAGGCTGTGAG 3009
Db 1779 TCCATCCCCAACTTCAATGACTTCTACATCGAGCTGGACGGCAACAACATGGGGGTGGAG 1838
QY 3010 TGCTTGGCGCTGCTCAAGAGATCATCGCTGATCTTGTGATGAGATTATCAGCGAGGAGCGG 3069
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Db 2019 GACTTGGCATTTGAGATGTTGACGTTCTGGATGAATCAACTACCACTTACCAACGAC 2078
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Db 2079 TTTGTCCTCCGAGTTGGCATCAATGTTGGCCCTGTGGTGGCTGGAGTGAATGGCCCTCGC 2138
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Db 2139 AGGCCCCAGTACGACATCTGGGGAAACAACAGTCAACGTGGCCAGTCCGATGGATGATAGACA 2198
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QY 3421 TACCAGCTGGAGTTCGAGGGGTGTCAAGGTGAAGGCAAGGGGAGATGACCACTTAC 3480
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QY 3481 TTCCTCAATGG 3491
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Db 2319 TTTCTAGAAGG 2329

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